

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:19:58 ; Search time 258 Seconds
(without alignments)
269.833 Million cell updates/sec

Title: US-09-529-206E-4
Perfect score: 959
Sequence: 1 MQAERGKGTGGTDADPGCG.....WITQCFLPVFLAQPSPGQRR 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	959	100.0	180	2 AAW62584	AAW62584 Cancer as
2	959	100.0	180	2 AAW69665	Aaw69665 Human NY-
3	959	100.0	180	2 AAY05965	Aay05965 Human can
4	959	100.0	180	3 AAY52430	Aay52430 Human tum
5	959	100.0	180	3 AAY70862	Aay70862 Human tum
6	959	100.0	180	3 AAB03154	Aab03154 Human oes
7	959	100.0	180	4 AAB69946	Aab69946 Human NY-
8	959	100.0	180	4 AAG67164	Aag67164 Amino aci
9	959	100.0	180	4 AAU01535	Aau01535 Human NY-
10	959	100.0	180	4 AAE07714	Aae07714 Human NY
11	959	100.0	180	5 AAU84818	Aau84818 Human NYN
12	959	100.0	180	5 AAU11543	Aau11543 Human tum
13	959	100.0	180	6 ABR58672	Abr58672 Human can
14	959	100.0	180	6 ABR48210	Abr48210 Human bla
15	959	100.0	180	6 ABUS6508	Abus6508 Lung canc
16	959	100.0	180	6 ABUS6694	Abus6694 Lung canc
17	959	100.0	180	6 ABP74198	Abp74198 Human NY-
18	959	100.0	180	6 ABR83438	Abr83438 Human NY-
19	959	100.0	180	7 ADC09576	Adc09576 NY-ESO-1
20	959	100.0	180	7 ADD35568	Add35568 Human NY-
21	959	100.0	180	7 ADD25510	Add25510 Binding d
22	959	100.0	180	7 ADN39068	Adn39068 Cancer/an
23	959	100.0	180	8 ADJ54139	Adj54139 Human NY-
24	959	100.0	180	8 ADM72815	Adm72815 Human NY-
25	959	100.0	180	8 ADQ18451	Adq18451 Human sof

26	959	100.0	180	8 ADQ10446	Adq10446 Autoimmun
27	959	100.0	397	4 AAE13122	Aae13122 NY-ESO-1C
28	953	99.4	180	6 ABU64816	Abu64816 Human NY-
29	950	99.1	180	8 ADM73418	Adm73418 CAG-3 pro
30	950	99.1	180	8 ADM73417	Adm73417 Human NY-
31	934.5	97.4	179	8 ADK68648	Adk68648 Epitope 1
32	918	95.7	180	7 ADD35564	Add35564 Human NY-
33	821	85.6	180	6 ABP74199	Abp74199 Human LAG
34	821	85.6	180	7 ADC09577	Adc09577 LAGE-1a p
35	821	85.6	180	8 ADM72816	Adm72816 Human LAG
36	814	84.9	180	2 AAW69664	Aaw69664 Human LAG
37	814	84.9	180	3 AAY70860	Aay70860 Human LAG
38	814	84.9	180	5 AAU84820	Aau84820 Human LAG
39	814	84.9	180	5 ABR78346	Abbr78346 Amino aci
40	814	84.9	180	7 ADC35103	Adc35103 Human bre
41	814	84.9	188	8 ADR66117	Adr66117 Human pro
42	814	84.9	188	8 ADR66459	Adr66459 Human pro
43	813	84.8	180	8 ADM73419	Adm73419 LAGE-1a p
44	808.5	84.3	179	8 ADM73424	Adm73424 Consensus
45	806	84.0	180	8 ADM73420	Adm73420 LAGE-1a p

ALIGNMENTS

RESULT 1
AAW62584
ID AAW62584 standard; protein; 180 AA.
XX
AC AAW62584;
XX
DT 17-SEP-1998 (first entry)
XX
DE Cancer associated antigen NY-ESO-1.
XX
KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 7 /note= "potential myristoylation site"
FT Misc-difference 9 /note= "potential myristoylation site"
FT Misc-difference 11 /note= "potential phosphorylation site"
FT Misc-difference 98 /note= "potential phosphorylation site"
FT Misc-difference 134 /note= "potential phosphorylation site"
FT Misc-difference 138 /note= "potential phosphorylation site"
XX
WO9814464-A1.
PN
PD 09-APR-1998.
XX
PF 15-SEP-1997; 97WO-US016335.
PR 03-OCT-1996; 96US-00725182.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;
PI Drifflouth JW;
XX
DR WPI; 1998-286417/25.
DR N-PSDB; AAV38566.
XX
PT New isolated cancer associated antigen - is used to develop products for
PT the diagnosis and treatment of cancers and for monitoring cancer therapy.
XX

CC The present sequence represents the ORF1 protein encoded by open reading
 CC frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and
 CC potent tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides comprising ORF1, ORF2 (see
 CC AAY05966), portions of these peptides and their variants (see AAY05965-
 CC 87), are useful as cancer vaccines that protect the recipient from
 CC development of cancer. The invention provides: vectors and host cells
 CC (also useful as vaccines); a method of diagnosis of cancer or precancer;
 CC a transgenic animal; antisense oligonucleotides that inhibit expression
 CC of the cancer peptide or tumour antigen; antibodies reacting with the CAG
 CC -3 cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 959; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGAGATGGRGPRGAGARASGPGGGA 60
 DB 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGAGATGGRGPRGAGARASGPGGGA 60
 QY 61 PRGPHGGAAGLNGCCRCGARGPESRLLEPYLAMPATPWEALARRSLAQDAPPLVPVG 120
 DB 61 PRGPHGGAAGLNGCCRCGARGPESRLLEPYLAMPATPWEALARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNIIITRLTADHRQLOLSLSSCLQQLSLMWITQCFPLVFLAQPPSGQRR 180
 DB 121 VLLKEFTVSGNIIITRLTADHRQLOLSLSSCLQQLSLMWITQCFPLVFLAQPPSGQRR 180

RESULT 4

AAY52430
 ID AAY52430 standard; protein; 180 AA.

XX AC AAY52430;

XX DT 21-OCT-2004 (revised)

XX DT 15-FEB-2000 (first entry)

XX DE Human tumour antigen NY-ESO-1.

XX KW Cancer; tumour; antigen; MHC; major histocompatibility complex; T-cell;
 KW cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
 KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
 KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.

XX OS Homo sapiens.
 XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Peptide 44..53
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 60..69
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 60..68
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 63..72
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 79..88
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 79..87
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide
 FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
 FT and HLA-B35"
 FT 82..91
 FT Peptide

FT Peptide
 FT /note= "Peptide presented by MHC Class I HLA-A1"
 FT 82..90
 FT /note= "Peptide presented by MHC Class I HLA-A1"
 FT 83..91
 FT /note= "Peptide presented by MHC Class I HLA-B44"
 FT 84..92
 FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
 FT and HLA-B35"
 FT 87..96
 FT /note= "Peptide presented by MHC Class I HLA-A1"
 FT 88..96
 FT /note= "Peptide presented by MHC Class I HLA-B44"
 FT 96..104
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT 100..108
 FT /note= "Peptide presented by MHC Class I HLA-B44"
 FT 102..110
 FT /note= "Peptide presented by MHC Class I HLA-B44"
 FT 107..116
 FT /note= "Peptide presented by MHC Class I HLA-A24"
 FT 110..118
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT 113..122
 FT /note= "Peptide presented by MHC Class I HLA-B7 and HLA-
 FT B52"
 FT 113..121
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT 115..124
 FT /note= "Peptide presented by MHC Class I HLA-A3"
 FT 118..126
 FT /note= "Peptide presented by MHC Class I HLA-B35"
 FT 124..133
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT 125..133
 FT /note= "Peptide presented by MHC Class I HLA-A24"
 FT 138..147
 FT /note= "Peptide presented by MHC Class I HLA-B8"
 FT 139..147
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT 145..153
 FT /note= "Peptide presented by MHC Class I HLA-A24 and HLA-
 FT B52"
 FT 153..162
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT 154..163
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT 154..162
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT 156..167
 FT /note= "Peptide (AAY52434) presented by MHC Class I HLA-
 FT A2"
 FT 158..166
 FT /note= "Peptide presented by MHC Class I HLA-A3"
 FT 159..167
 FT /note= "Peptide presented by MHC Class I HLA-A3"
 FT 162..170
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT
 XX WO959398-A1.
 XX
 XX 28-OCT-1999.
 XX
 XX 24-MAR-1999;
 XX 99WO-US006875.
 XX
 XX 17-APR-1998;
 XX 98US-00062422.
 XX 02-OCT-1998;
 XX 98US-00165546.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
 XX Gure A, Ritter G;
 XX WPI; 2000-038483/03.
 XX DR

DR N-PSDB; AAZ38380.
 XX
 XX Novel peptides which bind to MHC class I and MHC class II molecules,
 PT useful for therapeutic and diagnostic purposes.
 PS
 PS Claim 30; Fig 3; 49pp; English.
 XX
 XX This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
 CC encoding which was isolated from an oesophagus squamous cell cancer cDNA
 CC library. Tissue localisation studies revealed it to be expressed at high
 CC levels in normal ovary and testis but not in normal colon, kidney, liver,
 CC brain, oesophagus and skin. It was expressed in certain tumours and
 CC tumour cell lines with some degree of frequency - these included melanoma
 CC specimens and cell lines, and breast and bladder cancer specimens, with
 CC expression in other tumour types being sporadic. Peptides derived from NY
 CC -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
 CC and Class II molecules for presentation to T-cells. Peptides AAY52431-
 CC Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
 CC proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind
 CC to Class II HLA-DR3 molecules, stimulating helper T-cell proliferation.
 CC The peptides derived from NY-ESO-1 may be used in methods and
 CC compositions used for the treatment, diagnosis and prevention of cancers
 CC (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
 CC ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
 CC stimulate the proliferation of T cells
 CC
 CC Revised record issued on 21-OCT-2004 : Correction to feature table key
 XX
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 959; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 DB 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
 DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFLPVFLAQPSPGQRR 180
 DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFLPVFLAQPSPGQRR 180

RESULT 5
 AAY70862
 ID AAY70862 standard; protein; 180 AA.
 AC
 AC AAY70862;
 XX
 XX
 XX 31-JUL-2000 (first entry)
 DT
 DE Human tumour antigen, NY-ESO-1 protein.

XX NY-ESO-1; CAMEL; CTL-recognised Antigen on MELANOMA; human; cancer; CTL;
 KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
 KW melanoma; immunotherapy; immune response.
 XX
 OS Homo sapiens.
 XX
 XX WO200023584-A1.
 XX
 XX 27-APR-2000.
 PD
 PF 15-OCT-1999; 99WO-EP007832.
 XX
 XX 16-OCT-1998; 98EP-00119583.
 PR
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (UYHO-) UNIV HOSPITAL LEIDEN.

XX Schrier PI, Aarnoudse CA, Heider K, Klade C;
 PI
 XX WPI; 2000-339685/29.
 XX N-PSDB; AAD00152.
 XX
 PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
 PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
 XX
 PS Example 3; Page 62-63; 73pp; English.
 PS
 CC The present sequence is the human NY-ESO-1 protein, a tumour antigen,
 CC identified by screening an esophagus carcinoma cDNA library. This protein
 CC is derived from open reading frame (ORF)-1 that contain epitopes of
 CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
 CC but not in healthy tissues except in testis. It also shows homology with
 CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELANOMA)
 CC protein, a tumour-associated antigen. The tumour-associated antigen
 CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
 CC This sequence has anticancer activity. CAMEL tumour antigen and
 CC immunogenic peptides derived from it are useful for cancer immunotherapy.
 CC They have the potential to induce an immune response, by eliciting a CTL
 CC response. The DNA molecule is used for the construction of recombinant or
 CC fusion proteins
 XX
 XX Sequence 180 AA;

Query Match 100.0%; Score 959; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 DB 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
 DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFLPVFLAQPSPGQRR 180
 DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFLPVFLAQPSPGQRR 180

RESULT 6
 AAB03154
 ID AAB03154 standard; protein; 180 AA.
 AC
 AC AAB03154;
 XX
 XX 23-OCT-2000 (first entry)
 DT
 DE Human oesophageal cancer-associated antigen NY-ESO-1.
 XX
 XX Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
 KW oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
 KW antibody; diagnostic marker; drug delivery target.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 7
 FT /note= "Potential N-myristoylation site"
 FT Modified-site 9
 FT /note= "Potential N-myristoylation site"
 FT Modified-site 11
 FT /note= "Potential O-phosphorylation site"
 FT Modified-site 98
 FT /note= "Potential O-phosphorylation site"
 FT Modified-site 134
 FT /note= "Potential O-phosphorylation site"
 FT Modified-site 138
 FT /note= "Potential O-phosphorylation site"

FT Domain 152..172
 FT /note= "Potential transmembrane domain"
 PN US6069233-A.
 XX
 XX 30-MAY-2000.
 PD
 XX
 XX 26-JAN-1998; 98US-00013150.
 PF
 XX 03-OCT-1996; 96US-00725381.
 PR
 XX
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
 PI Old LJ;
 XX
 XX WPI; 2000-410880/35.
 DR N-PSDB; AAA61483.
 XX
 XX New isolated esophageal cancer-associated antigen useful as markers for
 XX producing antibodies and as targets for identifying abnormal conditions,
 XX e.g. infections and cancer.
 XX
 XX Example 5; Fig 3; 9pp; English.
 XX
 XX This sequence represents a human oesophageal cancer-associated antigen,
 CC NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
 CC library prepared from a specimen of well-to-moderately differentiated
 CC squamous cell cancer of the oesophagus. Expression analysis demonstrated
 CC that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
 CC cell lines and in normal ovary and testis tissue, but not in normal
 CC colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
 CC of the protein indicates that the protein has a transmembrane domain,
 CC several N-myristoylation sites and O-phosphorylation sites and that it
 CC contains antigenic sequences in the N-terminal half of the protein. The
 CC antigen is useful as an immunogen when combined with an adjuvant, in both
 CC precursor and post- translationally modified forms, and may be used to
 CC generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
 CC marker for oesophageal cancer, and can be utilised as a marker for the
 CC targetted delivery of therapeutic agents to oesophageal cancer cells. It
 CC can also be used to generate diagnostic or therapeutic agents
 XX
 XX Sequence 180 AA;
 SQ

Query Match 100.0%; Score 959; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRTGGSTGDADGGPGGPGIPDGGNAGGPGGAGATGGGPRGAGAAASGPGGGA 60
 Db 1 MQAEGRTGGSTGDADGGPGGPGIPDGGNAGGPGGAGATGGGPRGAGAAASGPGGGA 60
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
 Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPFLAQPSPGQRR 180
 Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPFLAQPSPGQRR 180

RESULT 7
 AAB69946
 ID AAB69946 standard; protein; 180 AA.
 XX
 XX AAB69946;
 AC
 XX
 XX 27-APR-2001 (first entry)
 DT
 XX
 XX Human NY-ESO-1 protein.
 DE
 XX

KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX
 XX Homo sapiens.
 XX WO200107917-A1.
 XX
 XX 01-FEB-2001.
 XX
 XX 14-JUL-2000; 2000WO-US019220.
 PF
 XX 23-JUL-1999; 99US-00359503.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 PI WPI; 2001-182822/18.
 DR N-PSDB; AAF58634.
 XX
 XX Method useful for determining the status (e.g. progression, regression or
 PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.
 XX
 XX Example 5; Fig 3; 50pp; English.
 XX
 XX The present sequence is human NY-ESO-1 protein. It is provided in a
 CC specification relating to a method for determining the status of a
 CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
 CC The method comprises assaying a sample taken from the patient for
 CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
 CC obtained to a prior value obtained from assay of a prior sample taken
 CC from the patient. Any difference between the values is indicative of a
 CC change in status of the cancerous condition. The method is useful for
 CC determining whether a cancerous condition is progressing, regressing or
 CC remaining stable, in particular in patients receiving treatment for a
 CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
 CC carcinoma
 XX
 XX Sequence 180 AA;
 SQ

Query Match 100.0%; Score 959; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRTGGSTGDADGGPGGPGIPDGGNAGGPGGAGATGGGPRGAGAAASGPGGGA 60
 Db 1 MQAEGRTGGSTGDADGGPGGPGIPDGGNAGGPGGAGATGGGPRGAGAAASGPGGGA 60
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
 Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPFLAQPSPGQRR 180
 Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPFLAQPSPGQRR 180

RESULT 8
 AAG67164
 ID AAG67164 standard; protein; 180 AA.
 XX
 XX AAG67164;
 AC
 XX
 XX 13-NOV-2001 (first entry)
 DT
 XX
 XX Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
 DE
 XX
 XX Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
 KW

KW HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
 KW cancer; testis tumour.
 XX
 XX Homo sapiens.
 XX
 PN WO200162917-A1.
 XX
 PD 30-AUG-2001.
 XX
 XX 22-JAN-2001; 2001WO-US002126.
 XX
 XX 22-FEB-2000; 2000US-00510635.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Lethe B, Boon-Falleur T;
 XX
 XX WPI; 2001-550091/61.
 DR N-PSDB; AAH75118.
 DR
 XX Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
 PT for diagnosing testicular tumors.
 PT
 XX Example 5; Fig 3; 50pp; English.
 XX
 XX The present sequence represents cancer testis tumour antigen NY-ESO-1
 CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
 CC least one human leukocyte antigen (HLA) binding peptide, which binds to
 CC Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
 CC expressed in tumour mRNA and in testis, but not normal colon, kidney,
 CC liver or brain tissue. The presence or level of expression of NY-ESO-1
 CC may be assayed for the diagnosis of cancer, especially testis tumours
 XX
 XX Sequence 180 AA;
 SQ
 Query Match 100.0%; Score 959; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5,2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 DB 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSISCCQLQLSLLMWITQCFLPVFLAQPSPGQRR 180
 DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSISCCQLQLSLLMWITQCFLPVFLAQPSPGQRR 180
 RESULT 9
 AAU01535
 ID AAU01535 standard; protein; 180 AA.
 AC AAU01535;
 XX
 XX 18-JUL-2001 (first entry)
 XX
 XX Human NY-ESO-1 tumour rejection antigen precursor protein.
 XX
 XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Modified-site 7
 FT /note= "Myristoylated"
 FT

FT Modified-site 9 /note= "Myristoylated"
 FT Modified-site 11 /note= "Phosphorylated"
 FT Modified-site 98 /note= "Phosphorylated"
 FT Modified-site 134 /note= "Phosphorylated"
 FT Modified-site 138 /note= "Phosphorylated"
 FT Modified-site 138 /note= "Phosphorylated"
 XX
 PN WO200123560-A2.
 XX
 XX 05-APR-2001.
 XX
 XX 26-SEP-2000; 2000WO-US026411.
 XX
 XX 29-SEP-1999; 99US-00408036.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Tureci O, Sahin U, Pfreundschuh M;
 PI
 XX WPI; 2001-266156/27.
 DR N-PSDB; AAS02254.
 DR
 XX
 XX Polypeptides binding to major histocompatibility complex class II human
 PT leukocyte antigen-determining region molecule having amino acid sequence
 PT found in tumor rejection antigen precursor used for stimulating
 PT proliferation of helper T cells.
 XX
 XX Claim 4; Fig 3; 62pp; English.
 XX
 XX The sequence represents a human NY-ESO-1 tumour rejection antigen
 CC precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
 CC major histocompatibility complex (MHC) Class II molecules such as human
 CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
 CC proliferation of helper T cells. The peptides can be administered to an
 CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
 CC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
 CC or present in free form is useful for this stimulation. The nucleic acid
 CC is useful for screening for a cancerous condition, which involves
 CC contacting a subject sample to a cell line transfected with the
 CC immunoreactive cell (helper T cell), where interaction is indicative of
 CC cancer. In addition, a sample from a patient (for example, a body fluid
 CC or tissue) can be monitored for the amount of the complex present in the
 CC bloodstream. This is useful for determining regression, progression or
 CC onset of a cancerous condition. The method involves contacting the sample
 CC with a radioactive labelled or enzyme labelled monoclonal antibody which
 CC specifically binds with the complex
 XX
 XX Sequence 180 AA;
 SQ
 Query Match 100.0%; Score 959; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5,2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 DB 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSISCCQLQLSLLMWITQCFLPVFLAQPSPGQRR 180
 DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSISCCQLQLSLLMWITQCFLPVFLAQPSPGQRR 180
 RESULT 10
 AAU07714
 ID AAU07714 standard; protein; 180 AA.

XX AC AAE07714;
 XX XX
 DT 06-NOV-2001 (first entry)
 XX XX
 DE Human NY ESO-1 protein.
 XX XX
 KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX XX
 OS Homo sapiens.
 XX XX
 XX Key Location/Qualifiers
 FT MISC-difference 45..47
 FT /note= "Encoded by CCGGGGCG"
 XX
 PN WO200155393-A2.
 XX XX
 XX 02-AUG-2001.
 XX XX
 XX 26-JAN-2001; 2001WO-US002765.
 XX XX
 XX 28-JAN-2000; 2000US-0179004P.
 XX 29-SEP-2000; 2000US-0237107P.
 XX XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX XX
 XX Wang R, Rosenberg SA, Zeng G;
 XX WPI; 2001-496851/54.
 XX N-PSDB; AAD14179, AAD14180.
 XX XX
 PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.
 XX XX
 XX Example 1; Fig 1; 134pp; English.
 XX XX
 CC The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC protein
 XX XX
 SQ Sequence 180 AA;
 Query Match 100.0%; Score 959; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRTGSGTDADGPGGPGIPDGGNAGGPGAGATGGRGPRGAGAAASGPGGA 60
 DB 1 MQAEGRTGSGTDADGPGGPGIPDGGNAGGPGAGATGGRGPRGAGAAASGPGGA 60
 QY 61 PRGPHGGAAGLNGCCRGARGPESRLLEFYLAMPATPMEALARRSLAQDAPPLPVPG 120
 DB 61 PRGPHGGAAGLNGCCRGARGPESRLLEFYLAMPATPMEALARRSLAQDAPPLPVPG 120

QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSISLQQLSLMLMTQCFLPVFLAQPSPGQR 180
 DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSISLQQLSLMLMTQCFLPVFLAQPSPGQR 180
 RESULT 11
 AAU84818
 ID AAU84818 standard; protein; 180 AA.
 XX AC AAU84818;
 XX XX
 DT 08-MAY-2002 (first entry)
 XX XX
 DE Human NYNSO1a consensus sequence.
 XX XX
 KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
 KW viral infection; human immunodeficiency virus; melanoma;
 KW bacterial infection; Salmonella; Legionella; parasitic infection;
 KW Trypanosoma; Toxoplasma; Giardia.
 XX XX
 OS Homo sapiens.
 XX XX
 PN WO200190197-A1.
 XX XX
 XX 29-NOV-2001.
 XX XX
 XX 25-MAY-2001; 2001WO-AU000622.
 XX XX
 XX 26-MAY-2000; 2000AU-00007761.
 XX XX
 XX (AUSU) UNIV AUSTRALIAN NAT.
 XX Thomson SA, Rameshaw IA;
 XX WPI; 2002-147575/19.
 XX XX
 PT New synthetic polypeptides having several different segments of at least
 PT one parent polypeptide linked together differently compared to the
 PT linkage in the parent polypeptide, for inducing immune response against a
 PT pathogen or cancer.
 XX XX
 PS Example 3; Fig 27; 364pp; English.
 CC The invention relates to a new synthetic polypeptide (I) comprising
 CC several different segments of at least one parent polypeptide linked
 CC together in a different relationship relative to their linkage in the
 CC parent polypeptide to impede, abrogate or otherwise alter at least one
 CC function associated with the parent polypeptide and for inducing an
 CC immune response against a pathogen or cancer. Also included are a
 CC synthetic polynucleotide encoding and a computer system for designing the
 CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
 CC are referred to as a Savine. The synthetic polypeptide is useful for
 CC modulating immune responses preferably directed against a pathogen or a
 CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
 CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
 CC oesophagus, brain, testicle, uterus), as potentiating agents.
 CC Compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcus, Haemophilus,
 CC Salmonella, Streptococcus, Legionella and Mycobacterium or parasitic
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
 CC a consensus sequence for a parent protein used to design a savine of the
 CC invention
 XX XX
 SQ Sequence 180 AA;
 Query Match 100.0%; Score 959; DB 5; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 XX therapeutic targets for screening drugs for treating these diseases.

PS Claim 12; Page 757-758; 767pp; English.

XX The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
 CC related gene nucleotide sequences which encode the proteins given in
 CC ABR59521 to ABR59709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 959; DB 6; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGGGPGIPDGGGNAGGPGAGATGGRGPRGAGAAASGPGGGA 60
 DB 1 MQAEGRTGSGTGDADGGGPGIPDGGGNAGGPGAGATGGRGPRGAGAAASGPGGGA 60
 QY 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 DB 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFPLVFLAQPSPGQRR 180
 DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFPLVFLAQPSPGQRR 180

RESULT 14

ABR48210
 ID ABR48210 standard; protein; 180 AA.

XX AC ABR48210;

XX DT 12-JUN-2003 (first entry)

XX DE Human bladder cancer associated protein sequence SEQ ID NO:139.

XX KW Human; bladder cancer; cytostatic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO2003003906-A2.

XX PD 16-JAN-2003.

XX PF 03-JUL-2002; 2002WO-US021338.

XX PR 03-JUL-2001; 2001US-0302814P.

XX PR 03-AUG-2001; 2001US-0310099P.

XX PR 08-NOV-2001; 2001US-0343705P.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PA (BOSB-) EOS BIOTECHNOLOGY INC.

XX

PI Mack DH, Aziz N;

XX WPI; 2003-201532/19.

DR N-PSDB; ACC51024.

XX Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.

XX Claim 10; Page 278; 307pp; English.

XX The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridizes to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 959; DB 6; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGGGPGIPDGGGNAGGPGAGATGGRGPRGAGAAASGPGGGA 60
 DB 1 MQAEGRTGSGTGDADGGGPGIPDGGGNAGGPGAGATGGRGPRGAGAAASGPGGGA 60
 QY 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 DB 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFPLVFLAQPSPGQRR 180
 DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFPLVFLAQPSPGQRR 180

RESULT 15

ABU56508
 ID ABU56508 standard; protein; 180 AA.

XX AC ABU56508;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polypeptide #101.

XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;

XX KW antinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;

XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

XX PN WO200286443-A2.

XX PD 31-OCT-2002.

XX PF 18-APR-2002; 2002WO-US012476.

XX PR 18-APR-2001; 2001US-0284770P.

XX PR 10-MAY-2001; 2001US-0290492P.

XX PR 09-NOV-2001; 2001US-0339245P.

PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
XX (BOSE-) EOS BIOTECHNOLOGY INC.
XX PA
XX PI Aziz N, Murray R;
XX
XX WI; 2003-093161/08.
DR N-PSDB; ABX76232.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
XX Claim 27; Page 270; 453pp; English.
PS
XX
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC invention
XX
SQ Sequence 180 AA;

Query Match		100.0%;	Score 959;	DB 6;	Length 180;
Best Local Similarity		100.0%;	Pred. No. 5.2e-79;		
Matches 180;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MQAEGRTGSGTGDADGPGGIPDGPFGNAGPGEAGATGGRGPRGAGARASGPGGGA 60			
Db	1	MQAEGRTGSGTGDADGPGGIPDGPFGNAGPGEAGATGGRGPRGAGARASGPGGGA 60			
Qy	61	PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPPATPWEALARRSLAQDAPPLPVP 120			
Db	61	PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPPATPWEALARRSLAQDAPPLPVP 120			
Qy	121	VLLKEFTVSGNLTIRLTAADHRQLQSLSSICLQQLSLLMWITQCFLPVFLAQPPSGQR 180			
Db	121	VLLKEFTVSGNLTIRLTAADHRQLQSLSSICLQQLSLLMWITQCFLPVFLAQPPSGQR 180			

Search completed: September 11, 2005, 01:38:04
Job time : 261 secs

J. Biol. Chem. 245, 5042-5048, 1970

A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens.

A;Reference number: A92069; MUID:71001508; PMID:4319110

A;Accession: A92069

A;Molecule type: protein

A;Residues: 263-268 <MOR>

A;Experimental source: skin

A;Note: Attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine

R;Labhard, M.E.; Hollister, D.W.

Matrix 10, 124-130, 1990

A;Title: Segmental amplification of the entire helical and telopeptide regions of the chicken type I procollagen

A;Reference number: S15989; MUID:90326017; PMID:2374517

A;Accession: S15989

A;Molecule type: mRNA

A;Residues: 281-302<LAB>

R;Wirtz, M.K.; Rao, V.H.; Glanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N.

Connect. Tissue Res. 29, 1-11, 1993

A;Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of type I procollagen

A;Reference number: I52905; MUID:93339042; PMID:8339541

A;Accession: I52905

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 342-352,'C',354-359 <W12>

A;Cross-references: GB:S64717; PIDN:G408195; PIDN:AB27677.1; PID:G408196

A;Note: Mutant sequence from patient with osteogenesis imperfecta

R;Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.

Biochemistry 22, 5213-5223, 1983

A;Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha 1(I) chain of type I procollagen

A;Reference number: A90476; MUID:84080385; PMID:6689127

A;Accession: A90476

A;Molecule type: mRNA

A;Residues: 425-1250,'X',1252-1328,'S',1330-1390,'X',1392-1464 <BER>

A;Cross-references: GB:X01328; NID:G180391; PIDN:AAA51995.1; PID:G180392

A;Note: sequence partially completed for missing nucleotides by A29439

R;Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.

J. Biol. Chem. 260, 691-694, 1985

A;Title: Multixon deletion in an osteogenesis imperfecta variant with increased type I(I) chain of type I procollagen

A;Reference number: A22161; MUID:85104934; PMID:2981843

A;Accession: A22161

A;Molecule type: DNA

A;Residues: 472-594,'R',596-607 <CH3>

A;Cross-references: GB:X03178; GB:X03179; NID:G179612; NID:G179613; PIDN:AAA51847.1; PID:G179613

A;Note: the authors translated the codon CGT for residue 595 as Pro

R;Wallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.

Am. J. Hum. Genet. 46, 1034-1040, 1990

A;Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained by a mutation in the alpha 1(I) chain of type I procollagen

A;Reference number: A35336; MUID:90252792; PMID:2339700

A;Accession: A35336

A;Molecule type: mRNA

A;Residues: 710-720,'E',722-737,'E',739-745 <WAL>

A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu

R;Forlino, A.; Zolerzi, F.; Valli, M.; Pignattelli, P.F.; Cetta, G.; Brunelli, P.C.; Mottes

Hum. Mol. Genet. 3, 2201-2206, 1994

A;Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the alpha 1(I) chain of type I procollagen

A;Reference number: I54365; MUID:95187161; PMID:7881420

A;Accession: I54365

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 746-766,'S',768-781 <FOR>

A;Cross-references: GB:I47667; NID:G1009093; PIDN:AA59576.1; PID:G1009094

R;Chesler, S.D.; Wallis, G.A.; Byers, P.H.

J. Biol. Chem. 268, 18218-18225, 1993

A;Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of type I procollagen

A;Reference number: A47426; MUID:93352646; PMID:8349697

A;Accession: A47426

A;Molecule type: mRNA

A;Residues: 1179-1276,'H',1278-1336,1339-1387,'R',1389-1464 <CHE>

A;Cross-references: GB:S64496; NID:G407589; PIDN:AB27856.1; PID:G407590

A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIPI:136445)

A;Note: does not represent an experimentally determined sequence but three different mutant sequences

A;Accession: B47426

A;Molecule type: mRNA

A;Residues: 1179-1464 <CH4>
A;Experimental source: normal dermal fibroblast culture
A;Accession: C47426
A;Molecule type: mRNA
A;Residues: 1179-1276,'H',1278-1464 <CH5>
A;Experimental source: fetal cell 86-237
A;Accession: D47426
A;Molecule type: mRNA
A;Residues: 1179-1336,1339-1464 <CH6>
A;Experimental source: fetal cell 86-146
A;Accession: E47426
A;Molecule type: mRNA
A;Residues: 1179-1387,R',1389-1464 <CH7>
A;Experimental source: fetal cell 88-251
R;Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nicol
J. Biol. Chem. 263, 14605-14607, 1988
A;Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide c
A;Reference number: I5269; MUID:89008319; PMID:3170557
A;Accession: I5269
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1187-1194,'C',1196-1220 <COH>
A;Cross-references: GB:M23213; NID:g340842; PIDN:AAB59363.1; PID:g499622
A;Note: mutant sequence from a patient with mild osteogenesis imperfecta
R;Maekelae, J.K.; Raassina, M.; Virita, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1988
A;Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.

Query Match 15.8%; Score 151.5; DB 1; Length 1464;
Best Local Similarity 37.2%; Pred.No.0.0006;
Matches 48; Conservative 4; Mismatches 42; Indels 35; Gaps 8;

QY 3 AEGR-GTGGSTGDA--DGPGGPGIPDPGGNAGGPGEGAGATGGRGPRGA----GAARASG 55
Db :|::|||:
825 AKSEPDGAKGDAGPFPAGPAGPPGPIGNVGAFAKAGSAGPGPATGPFGAAGRVG 884
:|::|||:

QY 56 P-----CGGAPRGPHGGAASGLGCCRCGARGESRLLEFYLLAMPFATPMELARRSLAQ 111
Db :|::|||:
885 PGPGSGNAGPPGPPGAG-----KEGGKPRGE-----TCPAGRPGEV----- 922

QY 112 DAPPLVPVG 120
Db |||||
923 -GPPGP-PG 929

RESULT 7
D70807
hypothetical glycine-rich protein RV3514 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: D70807
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70807
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1489 <COL>
A;Cross-references: GB:AL020223; GB:AL123456; NID:g3261554; PIDN:CAA17751.1; PID:g29244
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: RV3514
C;Superfamily: collagen alpha 1(IV) chain

Query Match 15.7%; Score 151; DB 2; Length 1489;
Best Local Similarity 41.1%; Pred.No.0.0006;
Matches 37; Conservative 2; Mismatches 31; Indels 20; Gaps 3;

QY 5 GRGTGGSTGDADGFGP-----GIPDPGGNAGGPGEA-----GATGGRGPRGA 48

Db 140 GAGAAAGCAGCGGPGAGLWNGNPGGAGSGGGTGGAGGAGGWLFGVGGAGVGAGG 199

Qy 49 GAARASGPG---GGAPRCPHCGAASGLNG 74

Db 200 GTGGAGGPGGLIWGGGGAGVGAGGGGTGG 229

RESULT 8

F70806
Hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: F70806
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Sqaers, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:96342230
A/Accession: F70806
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1901 <COL>
A/Cross-references: UNIPROT:O53553; GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA1774
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: Rv3508
C/Superfamily: collagen alpha 1(IV) chain

```

Query Match      15.7%; Score 151; DB 2; Length 1901;
Best Local Similarity 41.1%; Pred. No. 0.00082;
1 Matches 37; Conservative 2; Mismatches 20; Indels 20; Gaps 3;

QY      5  GRGTGGGTGADAGGGP-----GIPDGPGGNAGGPGEA-----GATGGRGPRGA 48
      |||:|||||
Db      140  GAGAAGAPGQAGGPGGAGLWNGGPGGAGSGGCTGAGGAGGWLFGVGGAGGVGGAGG 199

QY      49  GAARASPG-----CGAPRGPHGGAASGLNG 74

Db      200  GTGAGGPGGGLIWGGGGAGGVGGAGGCTGG 229

```

RESULT 9

T32812
hypothetical protein H17B01.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32812
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of *C. elegans* cosmid H17B01.
A:Reference number: Z11227
A:Accession: T32812
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-530 <GAT>
A:Cross-references: UNIPROT:O61209; EMBL:AF040646; PIDN:AAB94986.1; GSPDB:GN000020; CESP:
A:Experimental source: Strain Bristol N2; clone H17B01
C:Genetics:
A:Gene: CESP:H17B01.2
A:Map position: 2
A:Introns: 42/3; 58/1; 173/3; 268/2; 308/2; 340/1; 364/2; 387/3

Query Match	15.7%	Score 150.5;	DB 2;	Length 530;
Best Local Similarity	32.3%	Pred. No. 0.0002;		
Matches	51;	Conservative	9;	Mismatches 65; Indels 33; Gaps 8
Qy	5	GRGTGGSTGTDADPGCGPGI	PPGPGNAGGPGCEAGATCGRG-	PRGAGARASGPGGAPRG 63
Db	96	GLGTGPGNPGPGGLGTGPGP-	GTPGPGNPGGLGPGNPGGPTGPGGTGPGGPGH 154	

Qy	64	PHGGAAGL	NG	CCRC	GARGPESRLLEFVLAMP	ATPMEAE	106
Db	155	TAGTYIVII	VONGOR	IVNCAT	RLCCVGRNIT	VSVTDSVPPLVVTGP	207
Qy	107	RLSAQDAPPLV	PGVLLK	EFTVSGN	ILIRLT	138	
Db	208	SVTVTVPP	SPSVTF	GGRRPG	STPATFP	PGSVTVRYT	244

RESULT 10

H70589 hypotheetical glycine-rich protein Rv2853 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Mar-2003
C:Accession: H70589
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: H70589
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-615 <COL>
A:Cross-references: GB:Z95207; GB:AL123456; NID:g3261745; PID:CA808453.1; PID:e315182;
A:Experimental source: strain H37RV

Query Match	15.6%	Score 149.5	DB 2	Length 615
Best Local Similarity	49.3%	Pred. No. 0.00039		
Matches	35	Conservative 5	Mismatches 26	Indels 5
			Gaps	3

Qy	7	GTGGSTGDADGPGGFGIPDGGGNAGG--PGEAGATGGRGPRGA-GAARASGFGGGAPRG	63
		: : : : : : : : : :	
Db	532	GTGCGNGDGGGAGPGL--CGAGGAGGWLIIQSSTGCGGAGGAGGAGGAGSGGGAG	589
		: : : : : : : : :	
Qy	64	PHGGAASGLNG	74
Db	590	GHGDTTSGKNG	600

RESULT 11

T32734
myosin-IA - Acanthamoeba castellanii
C;Species: Acanthamoeba castellanii
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32734
R;Lee, W.L.; Ostap, E.M.; Zot, H.G.; Pollard, T.D.
submitted to the EMBL Data Library, August 1998
A;Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-IA GFA
A;Reference number: Z21216
A;Accession: T32734
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-1215 <LEE>
A;Cross-references: UNIPROT:O77202; EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAAC
A;Experimental source: strain Nefl
C;Genetics:
A;Gene: MTA
A;Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 236/1; 340/3; 390/3; 447/3; 500/3
C;Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homol
F;14-674/Domain: myosin motor domain homology <MMO>

Query Match 15.6%; Score 149.5; DB 2; Length 1215;
Best Local Similarity 41.0%; Pred. No. 0.00072;
Matches 41; Conservative 3; Mismatches 33; Indels 23; Gaps 4;

Qy 5 GRTGGGS-----TGDADPG-----GPGIPDPGGNAGGPGAGATGGRGP 45

Db 931 RGDKGTEGQDRGMKGHRGFSGLQGPFGPPGAPGEQGPSGASGPAG--PRGPPGSAGAA 988
Qy 71 ---GLNGC-CRCGARGPESRLLEFYLAMPPFATPWEAELARRSLAQDAPPLPVPGLLKEF 126
Db 989 GKDGLNGLPGPIGPPGPRGTGEVGPVGPFGPP-----GPRGP-EGPFSGGF 1034
Qy 127 TVSG 130
Db 1035 DLDG 1038

Search completed: September 11, 2005, 01:43:52
Job time : 52.5714 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:20:48 ; Search time 238.286 Seconds
(without alignments)
386.822 Million cell updates/sec

Title: US-09-529-206E-4

Perfect score: 959

Sequence: 1 MQAEGRGTCGTGDADPGG.....WITQCLPFLVLAQPPSGQRR 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	959	100.0	180	1 CTG1 HUMAN	P78358 homo sapien
2	595	62.0	210	1 CTG2 HUMAN	O75638 homo sapien
3	581	60.6	142	2 Q9NV13	Q9NV13 homo sapien
4	222	23.1	143	1 IBA2 HUMAN	Q14557 homo sapien
5	174.5	18.2	627	1 HYDL_STRCO	P42334 streptomyc
6	172.5	18.0	563	2 Q6J6N0	Q6J6N0 araneus ven
7	168.5	17.6	1002	2 Q9BTU8	Q9BTU8 argiope tri
8	167.5	17.5	922	2 O44367	O44367 mytilus edu
9	165.5	17.3	922	2 Q8MW53	Q8MW53 mytilus gal
10	162	16.9	420	2 Q6RF45	Q6RF45 arabidopsis
11	162	16.9	651	2 Q9BIU9	Q9BIU9 argiope tri
12	161	16.8	524	2 Q817U1	Q817U1 araneus ven
13	160.5	16.7	813	2 Q636W4	Q636W4 bacillus ce
14	160.5	16.7	1168	2 Q6HF99	Q6HF99 bacillus th
15	160.5	16.7	1408	2 Q7U022	Q7U022 mycobacteri
16	160.5	16.7	2249	2 Q9NHW4	Q9NHW4 nephila cla
17	160	16.7	604	2 Q9L252	Q9L252 streptomyc
18	160	16.7	871	2 Q44358	Q44358 nephila cla
19	159.5	16.6	1884	2 Q9NHW2	Q9NHW2 nephila ina
20	159	16.6	904	2 Q76271	Q76271 mytilus edu
21	158.5	16.5	678	2 Q93486	Q93486 oncorhynch
22	158.5	16.5	1458	2 Q16988	Q16988 araneus dia
23	157	16.4	410	2 Q16988	Q16988 araneus dia
24	157	16.4	626	2 Q9NHW1	Q9NHW1 nephila ina
25	156.5	16.3	1046	1 IF2_STRAW	Q82K53 streptomyc
26	155.5	16.2	145	2 Q61351	Q61351 drosophila
27	155.5	16.2	641	1 EBN1_EBV	P03211 epstein-bar
28	155.5	16.2	641	2 Q777E1	Q777E1 human herpe
29	155	16.2	894	2 Q8MW54	Q8MW54 mytilus gal
30	155	16.2	902	2 O16161	O16161 mytilus edu
31	154.5	16.1	478	2 Q81WX2	Q81WX2 bacillus an

32	154.5	16.1	481	2 Q6HV27	Q6HV27 bacillus an
33	154.5	16.1	905	2 Q8MW55	Q8MW55 mytilus gal
34	154.5	16.1	1953	2 Q9BIT7	Q9BIT7 nephila ina
35	153	16.0	1079	2 Q6MW7	Q6MW7 mycobacteri
36	153	16.0	1449	2 Q6NZ15	Q6NZ15 brachydanio
37	153	16.0	1449	2 Q6PE19	Q6PE19 brachydanio
38	152.5	15.9	734	2 Q6IVJ4	Q6IVJ4 ciona intes
39	152.5	15.9	779	1 CAIL1_BOVIN	P02453 bos taurus
40	152.5	15.9	1938	2 Q7TW00	Q7TW00 mycobacteri
41	152	15.8	219	2 Q9D9S4	Q9D9S4 mus musculu
42	152	15.8	610	2 Q9V5V8	Q9V5V8 drosophila
43	151.5	15.8	1715	2 Q8VIZ0	Q8VIZ0 mycobacteri
44	151.5	15.8	423	1 P041_HUMAN	Q01851 homo sapien
45	151.5	15.8	809	2 Q93485	Q93485 oncorhynch

ALIGNMENTS

RESULT 1

ID	CTG1_HUMAN	STANDARD;	PRT;	180 AA.
AC	P78358;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).			
DE	ESO-1.			
GN	Name=CTAG1B; Synonym=CTAG, CTAG1;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;			
RA	Chen Y.-T., Scanlan M.J., Sahin U., Tuerci O., Gure A.O., Tsang S.,			
RA	Williamson B., Stockert E., Pfeundscher M., Old L.J.;			
RT	"A testicular antigen aberrantly expressed in human cancers detected			
RT	by autologous antibody screening."			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Melanoma;			
RX	MEDLINE=98289662; PubMed=9626360;			
RA	Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,			
RA	de Flaen E., Boon T.;			
RT	"LAG-1, a new gene with tumor specificity."			
RL	Int. J. Cancer 76:903-908(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98430682; PubMed=9759882;			
RA	Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,			
RA	Schwarzenruber D.J., Rosenberg S.A.;			
RT	"A breast and melanoma-shared tumor antigen: T cell responses to			
RT	antigenic peptides translated from different open reading frames."			
RL	J. Immunol. 161:3596-3606(1998).			
CC	-!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide			
CC	variety of cancers. Detected in uterine myometrium.			
CC	-!- SIMILARITY: Belongs to the CTAG family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; U87459; AAB49693.1; -			
DR	EMBL; AU003149; CAA05908.1; -			
DR	EMBL; AF038567; AAD05202.1; -			
DR	Genew; HGNC:2491; CTAG1B.			

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DR  MIM; 300156; -.
KW  Antigen; Transmembrane.
FT  DOMAIN 5 82 Gly-rich.
FT  TRANSMEM 156 172 Potential.
SQ  SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 959; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.7e-58;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGAGATGGRGAGAAASGPGGGA 60
    |||||
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGAGATGGRGAGAAASGPGGGA 60
    |||||

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEALARRSLAQDAPPLVPVG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEALARRSLAQDAPPLVPVG 120

QY 121 VLLKFTVSGNLTIRLTAAHROQLSISSCLQQLSLMLWITQCLFVFLAQPSPGQR 180
Db 121 VLLKFTVSGNLTIRLTAAHROQLSISSCLQQLSLMLWITQCLFVFLAQPSPGQR 180

RESULT 2
ID CG2_HUMAN STANDARD; PRT; 210 AA.
AC O75637; O9BU80; O9U789; O9Y479;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN Names=CTAG2; Synonyms=ESO2, LAGE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
EX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LAGE-1A AND LAGE-1B).
RC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity." ;
RL Int. J. Cancer 76:903-908 (1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS GLN-6;
RP GLN-89 AND ARG-138.
RC TISSUE=Melanoma;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RL unexpected translation product of LAGE-1." ;
RN Int. J. Cancer 82:442-448 (1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LAGE-1B), AND VARIANT ARG-138.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.-I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalus D.E.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=LAGE-1B; Synonyms=LAGE-1L;
CC IsoId=O75638-1; Sequence=Displayed;
CC Name=LAGE-1A; Synonyms=LAGE-1S;
CC IsoId=O75638-2; Sequence=VSP_004301;
CC -!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
CC some uterus samples. Observed in 25-50% of tumor samples of
CC melanomas, non-small-cell lung carcinomas, bladder, prostate and
CC head and neck cancers.
CC -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
CC -!- SIMILARITY: Belongs to the CTAG family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ223093; CAA11117.1; -
DR EMBL; AJ223093; CAA11116.1; -
DR EMBL; AJ223040; CAA11043.1; -
DR EMBL; AJ223041; CAA11044.1; -
DR EMBL; AJ012834; CAA10194.1; -
DR EMBL; AJ012835; CAA10196.1; -
DR EMBL; BC002833; AA02833.1; -
DR Genew; HGNC:2492; CTAG2.
DR H-InvDB; HIX0017163; -.
DR MIM; 300396; -.
KW Alternative splicing; Antigen; Polymorphism; Transmembrane.
FT DOMAIN 5 79 Gly-rich.
FT DOMAIN 183 198 Poly-Pro.
FT VARSPLIC 135 210 MSVWDQDRGAGRMVVGVLGASPEGQKARDLTPKHV
FT FT SEORPTGPPPPGAGGDCRGVAFNVNFSAPHI -> IR
FT FT LTAADHROQLSISSCLQQLSLMLWITQCLFVFLAQPSPG
FT FT QRR (in isoform LAGE-1A).
FT FT /FTId=VSP_004301.
FT VARIANT 6 6 R -> Q.
FT FT /FTId=VAR_007855.
FT VARIANT 89 89 E -> Q.
FT FT /FTId=VAR_007856.
FT VARIANT 138 138 W -> R.
FT FT /FTId=VAR_007857.
FT FT /FTId=VAR_007857.
SQ SEQUENCE 210 AA; 21119 MW; 8BE0EE00AE55E8BE CRC64;

Query Match 62.0%; Score 595; DB 1; Length 210;
Best Local Similarity 82.0%; Pred. No. 3.4e-33;
Matches 109; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGAGATGGRGAGAAASGPGGGA 60
    |||||
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGAGATGGRGAGAAASGPGGGA 60
    |||||

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEALARRSLAQDAPPLVPVG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEALARRSLAQDAPPLVPVG 120

QY 121 VLLKFTVSGNLT 133
Db 121 AVLKDTVSGNLT 133

RESULT 3
Q9NY13 PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Hypoetical protein LAGE-2 (Fragment)
GN Name=LAGE-2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275978; CAB76945.1; -.
KW Hypoetical protein.
FT NON TER 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 60.6%; Score 581; DB 2; Length 142;
Best Local Similarity 94.8%; Pred. No. 2.1e-32;
Matches 109; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 27 PGNVAGPGAGATGGPRGAGAGARASPGGAPRPHGGAASGLNGCCRCGARGPESR 86
DB 1 PGNVAGPGAGATGGPRGAGAGARASPGGAPRPHGGAASGLNGCCRCGARGPESR 60
QY 87 LLEFYLLAMPATPMEAEARRSLAQDAPPLPVPGLVKEFTVSGNLTITRLTAAD 141
DB 1 LLEFYLLAMPATPMEAEARRSLAQDAPPLPVPGLVKEFTVSGNLTITRLTAAD 141
QY 61 LLEFYLLAMPATPMEAEARRSLAQDAPPLPVPGLVKEFTVSGNLTITVMSVQDD 115
DB 1 LLEFYLLAMPATPMEAEARRSLAQDAPPLPVPGLVKEFTVSGNLTITVMSVQDD 115

RESULT 4
IBA2 HUMAN STANDARD; PRT; 143 AA.
AC Q14657; O81278;
DT 01-NOV-1997 (Rel. 35, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE ITPA2 protein (ESO-3 protein) (DXS9879E).
GN Name=ITPA2; Synonyms=ESO3;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Blood, and Pancreas;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieff F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 2-143 FROM N.A., AND TISSUE SPECIFICITY.
RN TISSUE=Liver;
RC MEDLINE=96374823; PubMed=8786131; DOI=10.1006/geno.1996.0293;
RA Faranda S., Frattini A., Zucchi I., Patrosso C., Milanesi L.,
RA Montagna C., Vezzoni P.;

"Characterization and fine localization of two new genes in Xq28 using
the genomic sequence/EST database screening approach.";
Genomics 34:323-327(1996).
[3]
IDENTIFICATION AND TISSUE SPECIFICITY.
RP PubMed=12384295;
RX Alpen B., Guere A.O., Scanlan M.J., Old L.J., Chen Y.-T.;
RA "A new member of the NY-ESO-1 gene family is ubiquitously expressed in
RT somatic tissues and evolutionarily conserved.";
RL Gene 297:141-149(2002).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Belongs to the CTAG family.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to a
frameshift in position 54.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; BC015744; AAH15744.2; -.
CC EMBL; BC062330; AAH62330.1; -.
CC EMBL; X92896; CAA63489.1; ALT_FRAME.
CC MIM; 300060; -.
CC SEQUENCE 143 AA; 14804 MW; AD164559371449F8 CRC64;

Query Match 23.1%; Score 222; DB 1; Length 143;
Best Local Similarity 42.1%; Pred. No. 6.2e-08;
Matches 67; Conservative 14; Mismatches 52; Indels 26; Gaps 6;

QY 14 DADGPGGPGIPDGGGAGGPGGAGATGGPRGAGARASGPGGAP---RGPHGGAA 69
DB 3 DADADAG-----GGAGDGDG---GGHSCRG-GVDTAAAPAGAPPAHAPGGRDAA 50
QY 70 SGLNGCCRCGARGPESRLLEFYLLAMPATPMEAEARRSLAQDAPPLPVPGLVKEFTVS 129
DB 51 S-----AAGSRMRPHFTLSVFPPTLEAEIAHAGSLAPDAE--PHQRVVGKDLTVS 100
QY 130 GNILFRLTAADHRQLQLSISCLQLSLMMITQCFLP 168
DB 101 GRILVVRWKAEDCRLRLISVINFLDQLSLVVRTMORFGP 139

RESULT 5
HYDL STRCO STANDARD; PRT; 627 AA.
AC P42534; Q952L7;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative polyketide hydroxylase (EC 1.14.13.-) (WHIE ORF VIII).
GN OrderedLocusNames=SC05321; ORFNames=SC6G9.12c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz B., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
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DR	GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR	InterPro; IPR003979; tropoelastin.
DR	PRINTS; PR01500; TROP0ELASTIN.
FT	NON TER 1
SQ	SEQUENCE 563 AA; 46277 MW; D67BE594E296CA07 CRC64;
 Query Match 18.0%; Score 172.5; DB 2; Length 563; Best Local Similarity 46.5%; Pred. No. 0.00048; Matches 46; Conservative 1; Mismatches 27; Indels 25; Gaps 5	
Qy	5 GRGTGSGTGADGDGGPGCIPDPGCGNAGGPGEAGATGGRGPRGAGA-----50 156 GVPGGAPGAPGGPGGPGGPGGG-VGGPLGAGA-GGVGGGAGAYGPGGAGAYGPGGV 213
Dd	156 GVPGGAPGAPGGPGGPGGPGGG-VGGPLGAGA-GGVGGGAGAYGPGGAGAYGPGGV 213
Qy	51 ----ARASGPGGGAP--RGPHGGAASGLNGCCRCGARGP 83 214 GLGAGAYGFGAGPGGAGPHGPGGPGAG---PGGEGP 249
Dd	214 GLGAGAYGFGAGPGGAGPHGPGGPGAG---PGGEGP 249
 RESULT 7 Q9BIU8 PRELIMINARY; PRT; 1002 AA. ID Q9BIU8 AC Q9BIU8 DT 01-JUN-2001 (TrEMBLrel. 17, Created) DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) DE Flagelliform silk protein (Fragment). GN Name=Flag; OS Argiope trifasciata (Banded garden spider). OC Arachnida; Metazoa; Arthropoda; Chelicerata; Araneae; OC Araneomorphae; Entelegynae; Araneidae; Aranei; Argiope. NCBI_TaxID=156845; [1] RN RP SEQUENCE FROM N.A. RA Gatesy J.E., Hayashi C.Y.; RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL; AF350265; AAK30594.1; " GO; GO:0005737; C:cyttoplasm; IEA. DR GO; GO:0006817; P:phosphate transport; IEA. DR InterPro; IPR008160; Collagen. FT NON TER 1 FT NON TER 1002 1002 SQ SEQUENCE 1002 AA; 75889 MW; 432D73E1EDF6A89A CRC64;	
 Query Match 17.6%; Score 168.5; DB 2; Length 1002; Best Local Similarity 44.3%; Pred. No. 0.0015; Matches 43; Conservative 1; Mismatches 34; Indels 19; Gaps 3	
Qy	5 GRGTGSGTGADGDGGPGCIPDPGCGNAG-----GFGEAG----ATGGRGPRGA--48 141 CFGPGAPGARPGGPGGPGGPGGGVGGPGGAGYGGGVPACTGGFGPGGAGG 200
Dd	141 CFGPGAPGARPGGPGGPGGPGGGVGGPGGAGYGGGVPACTGGFGPGGAGG 200
Qy	49 ---GAARASGPGGAPRGPHGGAASGLNGCCRCGARG 82 201 FGPGGAGGFGGAGGFGGAGGYGPGGVPGGGAGG 237
Dd	201 FGPGGAGGFGGAGGFGGAGGYGPGGVPGGGAGG 237
 RESULT 8 O44367 PRELIMINARY; PRT; 922 AA. ID O44367 AC O44367; DT 01-JUN-1998 (TrEMBLrel. 06, Created) DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) DE Precollagen D.	


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ID Q7U022 PRELIMINARY; PRT; 1408 AA.
AC Q7U022;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PE-PGRS FAMILY PROTEIN.
GN Name=PE_PGRS27; OrderedLocusNames=Mb1485c;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248339; CAD96152.1; -.
DR InterPro; IPR000084; PE region_N.
DR InterPro; IPR002173; PfkB.
DR Pfam; PF00934; PE; 1.
DR ProDom; PD001223; PE_region_N; 1.
DR ProSITE; PS00583; PFKB_KINASES_1; UNKNOWN_2.
KW Complete proteome.
SQ SEQUENCE 1408 AA; 113412 MW; FF4C3685082F11CA CRC64;
* Query Match 16.7%; Score 160.5; DB 2; Length 1408;
* Best Local Similarity 44.7%; Pred. No. 0.007;
* Matches 42; Conservative 3; Mismatches 32; Indels 17; Gaps 4;
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Db 207 GGTGGAGGNAGLFGVGGTGGGGGGGGPGG-PGGPGVGGTGGAGGLGTLYGAGGH 265
QY 57 GGGAPRGP-----HG--GAASGLNGCCRCGARG 82
Db 266 GGAGGPGPIGGVGGHGGVGGAGLLGVGGHGGAG 299
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Search completed: September 11, 2005, 01:42:48
Job time : 240.286 secs

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GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: September 11, 2005, 01:30:14 ; Search time 66 Seconds
(without alignments)
203.588 Million cell updates/sec

Title: US-09-529-206E-4
Perfect score: 959
Sequence: 1 MQAEGRTGCGTGDADPGG.....WITQCFLPVFLAQPPSGRR 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	959	100.0	180	2	US-08-791-495-9
2	959	100.0	180	4	US-09-392-714-25
3	959	100.0	180	4	US-09-165-546D-15
4	959	100.0	180	4	US-09-341-829A-9
5	959	100.0	180	4	US-09-849-602-30
6	953	99.4	180	3	US-08-937-263B-8
7	953	99.4	180	4	US-09-751-798-8
8	814	84.9	180	2	US-08-791-495-7
9	814	84.9	180	4	US-09-341-829A-7
10	589	61.4	210	2	US-08-791-495-5
11	589	61.4	210	4	US-09-341-829A-5
12	160	16.7	745	2	US-09-010-928B-28
13	160	16.7	870	2	US-09-010-928B-2
14	156.5	16.3	633	1	US-08-642-255-73
15	156.5	16.3	1065	1	US-08-642-255-72
16	155.5	16.2	235	2	US-08-529-190B-1
17	155.5	16.2	641	4	US-09-249-585A-3
18	155.5	16.2	641	4	US-09-410-399-4
19	151.5	15.8	1057	3	US-08-931-820-1
20	151.5	15.8	1341	3	US-08-963-825-18
21	151.5	15.8	1341	3	US-09-500-811-18
22	151.5	15.8	1341	3	US-09-570-573-18
23	151.5	15.8	1341	3	US-09-548-608-18
24	151.5	15.8	1461	4	US-09-585-887-9
25	151.5	15.8	1461	4	US-09-289-578-9
26	151.5	15.8	1464	4	US-09-331-347C-21
27	150.5	15.7	907	2	US-09-010-928B-4

28	150	15.6	1008	3	US-09-219-849-8	Sequence 8, Appli
29	150	15.6	1065	1	US-08-642-255-80	Sequence 80, Appl
30	150	15.6	1065	3	US-08-642-246-16	Sequence 16, Appl
31	150	15.6	1065	4	US-09-451-206-16	Sequence 16, Appl
32	150	15.6	1065	5	PCT-US96-06229-16	Sequence 16, Appl
33	149	15.5	166	4	US-09-297-269-41	Sequence 41, Appl
34	148	15.4	857	4	US-09-902-540-12312	Sequence 12312, A
35	146.5	15.3	1806	4	US-09-919-497-56	Sequence 56, Appl
36	145	15.1	492	4	US-08-468-996-11	Sequence 11, Appl
37	145	15.1	1064	1	US-08-642-255-62	Sequence 62, Appl
38	142.5	14.9	1057	3	US-08-931-820-4	Sequence 4, Appli
39	142.5	14.9	1078	3	US-08-963-825-21	Sequence 21, Appl
40	142.5	14.9	1078	3	US-09-500-811-21	Sequence 21, Appl
41	142.5	14.9	1078	3	US-09-570-573-21	Sequence 21, Appl
42	142.5	14.9	1078	3	US-09-548-608-21	Sequence 21, Appl
43	141.5	14.8	1024	3	US-08-931-820-2	Sequence 2, Appli
44	141.5	14.8	1366	3	US-08-963-825-19	Sequence 19, Appl
45	141.5	14.8	1366	3	US-09-500-811-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P. C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-9

Query Match 100.0%; Score 959; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.6e-78;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGCGTGDADPGGIGIPDPGCGNAGCPGCGATGCGPRGAGAAASGPGGA 60
DB 1 MQAEGRTGCGTGDADPGGIGIPDPGCGNAGCPGCGATGCGPRGAGAAASGPGGA 60

QY 61 PRPHGGAAGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLPVP 120
Db 61 PRPHGGAAGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLPVP 120
QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQSLSSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAAADHRQLQSLSSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 2

US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; EARLIER FILING DATE: 1999-09-09
; EARLIER FILING DATE: PCT/US98/14679
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match 100.0%; Score 959; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.6e-78;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGGSTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGRTGGSTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRPHGGAAGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLPVP 120
Db 61 PRPHGGAAGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLPVP 120
QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQSLSSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAAADHRQLQSLSSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 3

US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM

OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6723832man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

Query Match 100.0%; Score 959; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.6e-78;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MQAEGRTGGSTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRPHGGAAGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLPVP 120
Db 61 PRPHGGAAGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLPVP 120
QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQSLSSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAAADHRQLQSLSSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 4

US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match 100.0%; Score 959; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.6e-78;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
DB 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLVPVG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
RESULT 5
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match 100.0%; Score 959; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.6e-78;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
DB 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLVPVG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 6
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ENCODING NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ISOLATED CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8
Query Match 99.4%; Score 953; DB 3; Length 180;
Best Local Similarity 99.4%; Pred. No. 5.6e-78;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
DB 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLVPVG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
RESULT 7
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 652517man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
;
US-09-751-798-8

Query Match          99.4%; Score 953; DB 4; Length 180;
Best Local Similarity 99.4%; Pred. No. 5.6e-78;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
DB 1 MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPLPVPG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPLPVPG 120
QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-791-495-7
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```
Query Match          84.9%; Score 814; DB 2; Length 180;
Best Local Similarity 84.4%; Pred. No. 1.6e-65;
Matches 152; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
DB 1 MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPLPVPG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPLPVPG 120
QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-341-829A-7

Query Match          84.9%; Score 814; DB 4; Length 180;
Best Local Similarity 84.4%; Pred. No. 1.6e-65;
Matches 152; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
DB 1 MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPLPVPG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPLPVPG 120
QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
;
US-08-791-495-5
```

```
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-5

; Query Match 61.4%; Score 589; DB 2; Length 210;
; Best Local Similarity 76.6%; Pred. No. 2.6e-45;
; Matches 108; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGGQTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMFPATPMEALARRSLAQDAPPLVPFG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMFPATPMEALARRSLAQDAPPLVPFG 120

QY 121 VLLKEFTVSGNLTIRLTAAD 141
Db 121 AVLKDFTVSGNLLFMSVRDQD 141

RESULT 12
US-09-010-928B-28
; Sequence 28, Application US/09010928B
; Patent No. 5994099
; GENERAL INFORMATION:
; APPLICANT: Lewis, Randolph V
; APPLICANT: Hayashi, Cheryl Y
; TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
; TITLE OF INVENTION: CODING THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 GATEHOUSE RD. SUITE 500E
; CITY: FALLS CHURCH
; STATE: VIRGINIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,928B
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M
; REGISTRATION NUMBER: 28977
; REFERENCE/DOCKET NUMBER: 1447-109P
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-010-928B-28

Query Match 16.7%; Score 160; DB 2; Length 745;
; Best Local Similarity 52.4%; Pred. No. 2.8e-06;
; Matches 43; Conservative 1; Mismatches 32; Indels 6; Gaps 5;

QY 5 GRGTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGG-GAPR 62
Db 508 GFGGFGGPGGFGGPGGAGGPGYGGG-AGGPGGAGGPGYGGAGG--PYGFGGAGGPGY 564

QY 63 GPHG-GAASGLNGCCRCGARGP 83
Db 565 GPGGAGGSGYGLGAGGSGGVGP 586

RESULT 13
US-09-010-928B-2
; Sequence 2, Application US/09010928B
; Patent No. 5994099
; GENERAL INFORMATION:
; APPLICANT: Lewis, Randolph V
; APPLICANT: Hayashi, Cheryl Y
; TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
```

```
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-5

; Query Match 61.4%; Score 589; DB 2; Length 210;
; Best Local Similarity 76.6%; Pred. No. 2.6e-45;
; Matches 108; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGGQTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMFPATPMEALARRSLAQDAPPLVPFG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMFPATPMEALARRSLAQDAPPLVPFG 120

QY 121 VLLKEFTVSGNLTIRLTAAD 141
Db 121 AVLKDFTVSGNLLFMSVRDQD 141

RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Fallieur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-341-829A-5

Query Match 61.4%; Score 589; DB 4; Length 210;
; Best Local Similarity 76.6%; Pred. No. 2.6e-45;
; Matches 108; Conservative 15; Mismatches 18; Indels 0; Gaps 0;
```

```
;
; TITLE OF INVENTION: CODING THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 GATEHOUSE RD. SUITE 500E
; CITY: FALLS CHURCH
; STATE: VIRGINIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M
; REGISTRATION NUMBER: 28977
; REFERENCE/DOCKET NUMBER: 1447-109P
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 870 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-010-928B-2

Query Match 16.7%; Score 160; DB 2; Length 870;
Best Local Similarity 52.4%; Pred. No. 3.3e-06;
Matches 43; Conservative 1; Mismatches 32; Indels 6; Gaps 5;

Qy 5 GRTGTGSTDADGGGGIPDGGNAGGP-GEAGATGGRGPRGAGAARASGPGG-GAPR 62
Db 634 GPGGFGGPGGFGGPGGAGGPGYFGG-AGGPGGAGGPGYGGAGG--PYGPGGAGGPY 690

Qy 63 GPHG-GAASGLNGCCRCGARGP 83
Db 691 GPGGAGGSGYGLGGAGSGGSGVGP 712

RESULT 14
US-08-642-255-73
; Sequence 73, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPELLO, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1065 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-642-255-72

Query Match 16.3%; Score 156.5; DB 1; Length 1065;
Best Local Similarity 41.7%; Pred. No. 8.6e-06;
Matches 43; Conservative 5; Mismatches 24; Indels 31; Gaps 6;
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-642-255-73

Query Match 16.3%; Score 156.5; DB 1; Length 633;
Best Local Similarity 41.7%; Pred. No. 4.8e-06;
Matches 43; Conservative 5; Mismatches 24; Indels 31; Gaps 6;

Qy 3 AEG-RGTGSGTD-----ADGPGGPG-----IPDGPGGNAGGPGSAGATGGRG 44
Db 107 AQPAGPGGSRGDPGPPGAQGPAGPGGSRGDPGPPGAQGPAGPGGSRGDPGPPGAHPAG 166

Qy 45 PRG-----AGAARASGPGGAPRGPHGGAASGLNGCCRCGARGP 83
Db 167 PKGAHPAGPKGAHPAG--PKGAHPAGPK-----GAQGP 200

RESULT 15
US-08-642-255-72
; Sequence 72, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPELLO, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1065 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-642-255-72

Query Match 16.3%; Score 156.5; DB 1; Length 1065;
Best Local Similarity 41.7%; Pred. No. 8.6e-06;
Matches 43; Conservative 5; Mismatches 24; Indels 31; Gaps 6;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2005, 01:43:05 ; Search time 243.429 Seconds
(without alignments)
291.657 Million cell updates/sec

Title: US-09-529-206E-4

Perfect score: 959

Sequence: 1 MQAERGTCGGTGDADGPGG.....WITQCFLPVLAQPPSGQRR 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1777461 segs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	959	100.0	180	10	US-09-849-602-30
2	959	100.0	180	14	US-10-207-655-71
3	959	100.0	180	15	US-10-026-066-3
4	959	100.0	180	15	US-10-117-937-74
5	959	100.0	180	15	US-10-295-027-386
6	959	100.0	180	15	US-10-296-734-832
7	959	100.0	180	15	US-10-188-832-139
8	959	100.0	180	16	US-10-777-053-11
9	959	100.0	180	16	US-10-751-088-15
10	959	100.0	180	16	US-10-657-022-74
11	959	100.0	180	16	US-10-837-217-11
					Sequence 30, Appl
					Sequence 71, Appl
					Sequence 3, Appl
					Sequence 74, Appl
					Sequence 386, App
					Sequence 832, App
					Sequence 139, App
					Sequence 11, Appl
					Sequence 15, Appl
					Sequence 74, Appl
					Sequence 11, Appl

12	959	100.0	180	16	US-10-877-373-9	Sequence 9, Appli
13	959	100.0	180	16	US-10-723-860-1270	Sequence 1270, Ap
14	959	100.0	180	17	US-10-871-708-7	Sequence 7, Appli
15	959	100.0	180	18	US-10-895-523-3	Sequence 3, Appli
16	959	100.0	180	18	US-10-182-506A-3	Sequence 3, Appli
17	959	100.0	180	18	US-10-756-149-5024	Sequence 5024, Ap
18	959	100.0	180	20	US-11-067-064-74	Sequence 74, Appl
19	959	100.0	397	9	US-09-821-883-27	Sequence 27, Appl
20	954	99.5	179	17	US-10-482-029-202	Sequence 202, App
21	953	99.4	180	9	US-09-751-798-8	Sequence 8, Appli
22	953	99.4	180	13	US-10-023-182-8	Sequence 8, Appli
23	918	95.7	180	14	US-10-364-614-14	Sequence 14, Appl
24	821	85.6	180	15	US-10-117-937-75	Sequence 75, Appl
25	821	85.6	180	16	US-10-657-022-75	Sequence 75, Appl
26	821	85.6	180	20	US-11-067-064-75	Sequence 75, Appl
27	814	84.9	180	14	US-10-146-473-69	Sequence 69, Appl
28	814	84.9	180	15	US-10-296-734-834	Sequence 834, App
29	814	84.9	180	16	US-10-468-406-4	Sequence 4, Appli
30	814	84.9	180	16	US-10-877-373-7	Sequence 7, Appli
31	631.5	65.8	135	15	US-10-295-027-388	Sequence 388, App
32	631.5	65.8	135	15	US-10-188-832-141	Sequence 141, App
33	596	62.1	210	14	US-10-157-031-88	Sequence 88, Appl
34	595	62.0	210	15	US-10-117-937-76	Sequence 76, Appl
35	595	62.0	210	16	US-10-657-022-76	Sequence 76, Appl
36	595	62.0	210	20	US-11-067-064-76	Sequence 76, Appl
37	589	61.4	210	16	US-10-877-373-5	Sequence 5, Appli
38	532	55.5	123	16	US-10-777-053-17	Sequence 17, Appl
39	532	55.5	123	16	US-10-837-217-17	Sequence 17, Appl
40	532	55.5	179	16	US-10-777-053-20	Sequence 20, Appl
41	532	55.5	179	16	US-10-837-217-20	Sequence 20, Appl
42	445	46.4	3541	15	US-10-296-734-1454	Sequence 1454, Ap
43	191	19.9	54	15	US-10-447-161-140	Sequence 140, App
44	172	17.9	30	15	US-10-296-734-1400	Sequence 1400, Ap
45	172	17.9	30	15	US-10-296-734-1432	Sequence 1432, Ap

ALIGNMENTS

RESULT 1
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Fseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match	100.0%;	Score 959;	DB 10;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 1.8e-67;		
Matches 180;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	61	PRGPHGGGAASGLNGCCRGARGPESRLLEFYLA	MPFATPMEALARRSLAQDAPPLVPVG	120
DB	61	PRGPHGGGAASGLNGCCRGARGPESRLLEFYLA	MPFATPMEALARRSLAQDAPPLVPVG	120
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RESULT 2
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-71

Query Match 100.0%; Score 959; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120

QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVLFAQPPSGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVLFAQPPSGQRR 180

RESULT 3
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPTOPE SYNCHRONIZATION IN ANTIGEN
; FILE REFERENCE: CTLIMM.21CPC
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match 100.0%; Score 959; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120

QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVLFAQPPSGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVLFAQPPSGQRR 180

RESULT 4
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match 100.0%; Score 959; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120

QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVLFAQPPSGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVLFAQPPSGQRR 180

RESULT 5
US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
```


APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 386
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-386

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Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQADAPLPVPG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSCLQLSLMLWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSCLQLSLMLWITQCFLPVFLAQPSPGQRR 180

RESULT 6
US-10-296-734-832
Sequence 832, Application US/10296734
Publication No. US20040054137A1
GENERAL INFORMATION:
APPLICANT: Thompson, Scott A
APPLICANT: Ramshaw, Ian A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU PQ7761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PatentIn version 3.2
SEQ ID NO 832
LENGTH: 180
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: NYNsola consensus polypeptide

US-10-296-734-832
Query Match 100.0%; Score 959; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGA 60
DB 1 MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQADAPLPVPG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQADAPLPVPG 120
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RESULT 7
US-10-188-832-139
Sequence 139, Application US/10188832
Publication No. US20040076955A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Azi, Natasha
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002330US
CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 60/302,814
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 139
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 959; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQADAPLPVPG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQADAPLPVPG 120
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RESULT 8
US-10-777-053-11
Sequence 11, Application US/10777053
Publication No. US20040132088A1
GENERAL INFORMATION:

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; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANKK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-777-053-11

Query Match 100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MQAEGRTGSGTDADGPGGPGIPDGPNGAGGPGAGATGGRPGAGAAASGPGGGA 60
QY 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
Db 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCQLQLSLLMWITQCFLPVFLAOPPSGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCQLQLSLLMWITQCFLPVFLAOPPSGQRR 180

RESULT 9
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/751,088
; FILING DATE: 02-Jan-2004
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
```

```
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15

Query Match 100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTDADGPGGPGIPDGPNGAGGPGAGATGGRPGAGAAASGPGGGA 60
Db 1 MQAEGRTGSGTDADGPGGPGIPDGPNGAGGPGAGATGGRPGAGAAASGPGGGA 60
QY 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
Db 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCQLQLSLLMWITQCFLPVFLAOPPSGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCQLQLSLLMWITQCFLPVFLAOPPSGQRR 180

RESULT 10
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANKK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-657-022-74

Query Match 100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTDADGPGGPGIPDGPNGAGGPGAGATGGRPGAGAAASGPGGGA 60
Db 1 MQAEGRTGSGTDADGPGGPGIPDGPNGAGGPGAGATGGRPGAGAAASGPGGGA 60
QY 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
Db 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCQLQLSLLMWITQCFLPVFLAOPPSGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCQLQLSLLMWITQCFLPVFLAOPPSGQRR 180
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RESULT 11
US-10-837-217-11
; Sequence 11, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-837-217-11

Query Match 100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
DB 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPPATPMEAEALARRSLAQDAPPLPVP 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPPATPMEAEALARRSLAQDAPPLPVP 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSICLQLSLMWITQCFLPVLAPPPSGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSICLQLSLMWITQCFLPVLAPPPSGQRR 180

RESULT 12
US-10-877-373-9
; Sequence 9, Application US/10877373
; Publication No. US20040234541A1
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/10/877,373
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/05/341,829
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-877-373-9

Query Match 100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
DB 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPPATPMEAEALARRSLAQDAPPLPVP 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPPATPMEAEALARRSLAQDAPPLPVP 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSICLQLSLMWITQCFLPVLAPPPSGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSICLQLSLMWITQCFLPVLAPPPSGQRR 180

RESULT 13
US-10-723-860-1270
; Sequence 1270, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; METHODS FOR SCREENING FOR SOFT TISSUE SARCOMA MODULATORS
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1270
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-1270

Query Match 100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
DB 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPPATPMEAEALARRSLAQDAPPLPVP 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPPATPMEAEALARRSLAQDAPPLPVP 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSICLQLSLMWITQCFLPVLAPPPSGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSICLQLSLMWITQCFLPVLAPPPSGQRR 180

RESULT 14
US-10-871-708-7
; Sequence 7, Application US/10871708
; Publication No. US20050118186A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.035A
; CURRENT APPLICATION NUMBER: US/10/871,708
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: 60/479,554
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Autoimmunogenic Cancer
US-10-871-708-7

Job time : 244.429 secs

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Query Match      100.0%; Score 959; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAARASGPGGGA 60
    |||||||
Db   1  MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAARASGPGGGA 60
    |||||||
QY  61  PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
    |||||||
Db   61  PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
    |||||||
QY  121  VLLKEFTVSGNLTIRLTADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAOPPSGQRR 180
    |||||||
Db   121  VLLKEFTVSGNLTIRLTADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAOPPSGQRR 180
    |||||||
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RESULT 15

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US-10-895-523-3
; Sequence 3, Application US/10895523
; Publication No. US20050130920A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Lei, Xiang-Dong
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: MANNK.021C1PCCI
; CURRENT APPLICATION NUMBER: US/10/895,523
; CURRENT FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: 10/026,066
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/005,905
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/999,186
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-895-523-3
```

```
Query Match      100.0%; Score 959; DB 18; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAARASGPGGGA 60
    |||||||
Db   1  MQAEGRTGGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAARASGPGGGA 60
    |||||||
QY  61  PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
    |||||||
Db   61  PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
    |||||||
QY  121  VLLKEFTVSGNLTIRLTADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAOPPSGQRR 180
    |||||||
Db   121  VLLKEFTVSGNLTIRLTADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAOPPSGQRR 180
    |||||||
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Search completed: September 11, 2005, 02:07:10

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:19:58 ; Search time 28.6667 Seconds
(without alignments)
269.833 Million cell updates/sec

Title: US-09-529-206E-4_COPY_43_62

Perfect score: 107

Sequence: 1 RGRPGAGARASFGGGAPR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	20	2	AAY05979 Human can
2	107	100.0	179	8	ADK68648 Epitope 1
3	107	100.0	180	2	Aaw62584 Cancer as
4	107	100.0	180	2	Aaw69665 Human NY-
5	107	100.0	180	2	AAY05965 Human can
6	107	100.0	180	3	AAY52430 Human tum
7	107	100.0	180	3	AAY70862 Human tum
8	107	100.0	180	3	AAB03154 Human oes
9	107	100.0	180	4	AAB69946 Human NY-
10	107	100.0	180	4	AAG67164 Amino aci
11	107	100.0	180	4	AAU01535 Human NY-
12	107	100.0	180	4	AAE07714 Human NY-
13	107	100.0	180	5	AAU84818 Human NYN
14	107	100.0	180	5	AAU11543 Human tum
15	107	100.0	180	6	ABR58672 Human can
16	107	100.0	180	6	ABR48210 Human bla
17	107	100.0	180	6	ABU56508 Lung can
18	107	100.0	180	6	ABU56694 Lung can
19	107	100.0	180	6	ABP74198 Human NY-
20	107	100.0	180	6	ABR34338 Human NY-
21	107	100.0	180	7	ADC09576 NY-ESO-1
22	107	100.0	180	7	ADD35568 Human NY-
23	107	100.0	180	7	ADD25510 Binding d
24	107	100.0	180	7	ADN39068 Cancer/an
25	107	100.0	180	8	ADJ54139 Human NY-

26	107	100.0	180	8	ADM72815	Adm72815 Human NY-
27	107	100.0	180	8	ADM73418	Adm73418 CAG-3 pro
28	107	100.0	180	8	ADM73417	Adm73417 Human NY-
29	107	100.0	180	8	ADQ18451	Adq18451 Human sof
30	107	100.0	180	8	ADQ10446	Adq10446 Autoimmun
31	107	100.0	397	4	AAE13122	AAE13122 NY-ESO-IC
32	102	95.3	30	5	AAU85105	AAU85105 Human NYN
33	102	95.3	3541	5	AAU85130	AAU85130 Human mel
34	101	94.4	180	6	ABU64816	ABU64816 Human NY-
35	101	94.4	180	7	ADU35564	ADU35564 Human NY-
36	99	92.5	135	6	ABR58673	ABR58673 Human can
37	99	92.5	135	6	ABR48211	ABR48211 Human bla
38	99	92.5	135	6	ABU56509	ABU56509 Lung can
39	99	92.5	135	6	ABU56695	ABU56695 Lung can
40	99	92.5	135	7	ADN39070	ADN39070 Cancer/an
41	99	92.5	179	8	ADM73424	ADM73424 Consensus
42	99	92.5	180	2	AAW69664	AAW69664 Human LAG
43	99	92.5	180	3	AAU70860	AAU70860 Human LAG
44	99	92.5	180	5	AAU84820	AAU84820 Human LAG
45	99	92.5	180	5	ABB78346	ABB78346 Amino aci

ALIGNMENTS

RESULT 1
AAY05979
ID AAY05979 standard; peptide; 20 AA.
AC AAY05979;
XX
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Wang RF, Rosenberg SA;
XX
DR WPI, 1999-277270/23.
PT
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 16; Page 64; 88pp; English.
XX
CC The present sequence represents a cancer peptide that is based on amino
CC acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AA05965),
CC a new and potent tumour antigen capable of eliciting an antigen specific
CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
CC 87), are useful as cancer vaccines that protect against cancer. The
CC invention provides: vectors and host cells (also useful as vaccines); a
CC method of diagnosis of cancer or precancer; a transgenic animal;
CC antisense oligonucleotides that inhibit expression of the cancer peptide

CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
 CC useful in diagnostic and detection assays; and methods for preventing or
 CC inhibiting cancer by administering a cancer peptide, with or without an
 CC HLA molecule. The cancer peptides form part of, or are derived from,
 CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
 CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
 CC inducing cancer-specific T cells in vitro for subsequent return to a
 CC patient
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 107; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPGRGAGARASGPGGGAPR 20
 |||||
 Db 1 RGPGRGAGARASGPGGGAPR 20

RESULT 2
 ADK68648
 ID ADK68648 standard; protein; 179 AA.
 XX
 AC ADK68648;

XX
 DT 06-MAY-2004 (first entry)
 XX

XX Epitope liberation-related NY-ESO-1 protein SeqID11.

XX epitope liberation; substrate; proteasome; cytostatic; antibacterial;
 KW protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
 KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
 KW virus; bacterium; protozoan; fungus; housekeeping proteasome system;
 KW human.

XX Homo sapiens.

XX US2003228634-A1.

XX 11-DEC-2003.

XX 07-NOV-2002; 2002US-00292413.

XX 07-NOV-2001; 2001US-0336968P.

XX (SIMA/) SIMARD J J L.

XX (DIAM/) DIAMOND D C.

XX (QIUZ/) QIU Z.

XX (LEIX/) LEI X.

XX Simard JUL, Diamond DC, Qiu Z, Lei X;

XX WPI; 2004-167209/16.

XX N-PSDB; ADK68674.

XX Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
 PT liberation by contacting substrate polypeptide comprising epitope of
 PT interest, with proteasome, and assaying for liberation of epitope.

XX Example 2; SEQ ID NO 11; 67pp; English.

XX This invention relates to a novel method of identifying a polypeptide
 CC suitable for epitope liberation, including the steps of identifying an
 CC epitope of interest; providing substrate polypeptide sequence including
 CC the epitope, wherein the substrate permits processing by a proteasome;
 CC contacting the substrate with a composition including the proteasome,
 CC under conditions that support processing of the substrate by proteasome;
 CC and assaying for liberation of epitope. The invention may be useful for
 CC the development of compounds with a cytostatic, antibacterial,
 CC protozoacide or fungicide activity acting as T-cell activators. In

CC addition, the invention may allow development of a vaccine. The invention
 CC is useful for identifying a polypeptide suitable for epitope liberation,
 CC where the epitope is a housekeeping epitope. The compositions comprising
 CC the identified housekeeping epitopes are useful in vitro in vaccine
 CC development or in the generation or expansion of cytotoxic T lymphocyte
 CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
 CC for activating T-cells against neoplastic cells, and cells infected with
 CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
 CC on the knowledge that such epitopes are, in fact, produced by the
 CC housekeeping proteasome system. Once identified, these epitopes, embodied
 CC as peptides, can be used to successfully immunise or induce therapeutic
 CC CTL responses against housekeeping proteasome expressing target cells in
 CC the host. The present sequence is that of a protein which is related to
 CC the method of the invention.

XX Sequence 179 AA;

Query Match 100.0%; Score 107; DB 8; Length 179;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPGRGAGARASGPGGGAPR 20
 |||||
 Db 42 RGPGRGAGARASGPGGGAPR 61

RESULT 3
 AAW62584
 ID AAW62584 standard; protein; 180 AA.
 XX

XX AAW62584;

XX 17-SEP-1998 (first entry)

XX Cancer associated antigen NY-ESO-1.

XX Cancer associated antigen; NY-ESO-1; regression; progression; onset;
 KW cancer; treatment; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 7 /note= "potential myristoylation site"

FT Misc-difference 9 /note= "potential myristoylation site"

FT Misc-difference 11 /note= "potential phosphorylation site"

FT Misc-difference 98 /note= "potential phosphorylation site"

FT Misc-difference 134 /note= "potential phosphorylation site"

FT Misc-difference 138 /note= "potential phosphorylation site"

XX WO9814464-A1.

XX 09-APR-1998.

XX 15-SEP-1997; 97WO-US016335.

XX 03-OCT-1996; 96US-00725182.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;

XX Drijfhout JW;

XX WPI; 1998-286417/25.

XX N-PSDB; AAV38566.

XX New isolated cancer associated antigen - is used to develop products for
 PT the diagnosis and treatment of cancers and for monitoring cancer therapy.

XX Claim 8; Fig 3; 49pp; English.

XX The present sequence represents a cancer associated antigen. The clone

CC from which the DNA sequence is obtained is designated NY-ESO-1. The

CC specification described a method for determining regression, progression

CC of onset of a cancerous condition, comprising monitoring a sample from a

CC patient with the cancerous condition for a parameter selected from NY-ESO

CC -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells

CC specific for the peptide and an MHC molecule with which it non-covalently

CC complexes. Methods for the treatment of a cancerous condition are also

CC described. The NY-ESO-1 protein and peptides derived from it can be used

CC for diagnosis and treatment of cancers and to monitor the efficacy of a

CC therapeutic regime

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20

DB 43 RGRPGAGAAASGPGGGAPR 62

RESULT 4

AAW69665

ID AAW69665 standard; protein; 180 AA.

XX AC AAW69665;

XX DT 27-OCT-1998 (first entry)

XX Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.

XX Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

XX Homo sapiens.

XX WO9832855-A1.

XX 30-JUL-1998.

XX 27-JAN-1998; 98WO-US001445.

XX 27-JAN-1997; 97US-00791495.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Lethe B, Lucas S, De Smet C, Godelaine D, Boon-Palleur T;

XX WPI: 1998-427951/36.

XX N-PSDB; AAV50348.

XX New isolated LAGE-1 tumour associated nucleic acids - used to develop

PT products for the diagnosis and treatment of LAGE-1 associated disorders,

PT particularly tumours.

XX Example 2; Page 57-58; 73pp; English.

XX The present sequence represents human NY-ESO-1, formerly known as LL-1.2

CC clone, which is used in an example from the present invention which

CC describes LAGE-1 tumour associated protein (TAP). The present invention

CC also describes: (1) a method for treating a subject with a disorder

CC characterised by expression of a LAGE-1 nucleic acid molecule or an

CC expression product, comprising administering to the subject autologous

CC cytolytic T cells to ameliorate the disorder, where the cytolytic T cells

CC are specific for complexes of an HLA molecule and a LAGE-1 TAP or an

CC immunogenic fragment; (2) a method for treating a subject with a disorder

CC characterised by expression of a LAGE-1 nucleic acid molecule or an

CC expression product, comprising administering a LAGE-1 TAP or an

CC immunogenic fragment to ameliorate the disorder; and (3) a method for

CC selectively enriching a population of T cells with cytolytic T cells

CC specific for a LAGE-1 TAP comprising contacting an isolated population of

CC T cells with an agent presenting a complex of a LAGE TAP or an

CC immunogenic fragment and a HLA presenting molecule to selectively enrich

CC the isolated population of T cells with the cytolytic T cells. The

CC methods and products from the present invention can be used for the

CC diagnosis and treatment of LAGE-1 associated disorders, particularly

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20

DB 43 RGRPGAGAAASGPGGGAPR 62

RESULT 5

AAV05965

ID AAV05965 standard; protein; 180 AA.

XX AC AAV05965;

XX DT 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;

XX non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis;

XX melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer;

XX breast cancer; prostate cancer; ovarian cancer; cervical cancer;

XX bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;

XX tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.

XX Homo sapiens.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI: 1999-277270/23.

XX N-PSDB; AAX58599.

XX Cancer antigen NY ESO1/CAG-3.

XX Claim 4; Fig 3A; 88pp; English.

XX The present sequence represents the ORF1 protein encoded by open reading

CC frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and

CC potent tumour antigen capable of eliciting an antigen specific immune

CC response by T cells. Cancer peptides comprising ORF1, ORF2 (see

CC AAY05966), portions of these peptides and their variants (see AAY05965-

CC 87), are useful as cancer vaccines that protect the recipient from

CC development of cancer. The invention provides: vectors and host cells

CC (also useful as vaccines); a method of diagnosis of cancer or precancer;

CC a transgenic animal; antisense oligonucleotides that inhibit expression

CC of the cancer peptide or tumour antigen; antibodies reacting with the CAG

CC -3 cancer peptide, useful in diagnostic and detection assays; and methods

CC for preventing or inhibiting cancer by administering a cancer peptide,

CC with or without an HLA molecule. The cancer peptides form part of, or are

CC derived from, cancers such as primary or metastatic melanoma, thymoma,

CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

CC ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
 CC simulate the proliferation of T cells

CC Revised record issued on 21-OCT-2004 : Correction to feature table key

XX Sequence 180 AA;

Query Match 100.0%; Score 107; DB 3; Length 180;

Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGPGGAPR 20

DB 43 RGRGAGAAARASGPGGAPR 62

RESULT 7

AAAY70862

ID AAY70862 standard; protein; 180 AA.

XX AC AAY70862;

XX DT 31-JUL-2000 (first entry)

XX DE Human tumour antigen, NY-ESO-1 protein.

XX KW NY-ESO-1; CAMEL; CTL-Recognised Antigen on MELanoma; human; cancer; CTL;
 KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
 KW melanoma; immunotherapy; immune response.

XX OS Homo sapiens.

XX PN WO200023584-A1.

XX PD 27-APR-2000.

XX PF 15-OCT-1999; 99WO-EP007832.

XX PR 16-OCT-1998; 98EP-00119583.

XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX PA (UYHO-) UNIV HOSPITAL LEIDEN.

XX PI Schrier PI, Aarnoudse CA, Heider K, Klade C;

XX WPI; 2000-339685/29.

XX DR N-PSDB; AAD00152.

XX PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
 the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.

XX PS Example 3; Page 62-63; 73pp; English.

XX CC The present sequence is the human NY-ESO-1 protein, a tumour antigen,
 CC identified by screening an esophagus carcinoma cDNA library. This protein
 CC is derived from open reading frame (ORF)-1 that contain epitopes of
 CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
 CC but not in healthy tissues except in testis. It also shows homology with
 CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
 CC protein, a tumour-associated antigen. The tumour-associated antigen
 CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
 CC This sequence has anticancer activity. CAMEL tumour antigen and
 CC immunogenic peptides derived from it are useful for cancer immunotherapy.
 CC They have the potential to induce an immune response, by eliciting a CTL
 CC response. The DNA molecule is used for the construction of recombinant or
 CC fusion proteins

XX Sequence 180 AA;

Query Match 100.0%; Score 107; DB 3; Length 180;

Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGPGGAPR 20

DB 43 RGRGAGAAARASGPGGAPR 62

RESULT 8

AAB03154

ID AAB03154 standard; protein; 180 AA.

XX AC AAB03154;

XX DT 23-OCT-2000 (first entry)

XX DE Human oesophageal cancer-associated antigen NY-ESO-1.

XX KW Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
 KW oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
 KW antibody; diagnostic marker; drug delivery target.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 7 /note= "Potential N-myristoylation site"

FT Modified-site 9 /note= "Potential N-myristoylation site"

FT Modified-site 11 /note= "Potential O-phosphorylation site"

FT Modified-site 98 /note= "Potential O-phosphorylation site"

FT Modified-site 134 /note= "Potential O-phosphorylation site"

FT Modified-site 138 /note= "Potential O-phosphorylation site"

FT Domain 152..172 /note= "Potential transmembrane domain"

XX US6069233-A.

XX 30-MAY-2000.

XX 26-JAN-1998; 98US-00013150.

XX 03-OCT-1996; 96US-00725381.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX (CORR) CORNELL RES FOUND INC.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
 PI Old LJ;

XX WPI; 2000-410880/35.

XX N-PSDB; AAA61483.

XX New isolated esophageal cancer-associated antigen useful as markers for
 producing antibodies and as targets for identifying abnormal conditions,
 e.g. infections and cancer.

XX Example 5; Fig 3; 9pp; English.

XX This sequence represents a human oesophageal cancer-associated antigen,
 CC NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
 CC library prepared from a specimen of well-to-moderately differentiated
 CC squamous cell cancer of the oesophagus. Expression analysis demonstrated
 CC that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
 CC cell lines and in normal ovary and testis tissue, but not in normal
 CC colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
 CC of the protein indicates that the protein has a transmembrane domain,
 CC several N-myristoylation sites and O-phosphorylation sites and that it
 CC contains antigenic sequences in the N-terminal half of the protein. The
 CC antigen is useful as an immunogen when combined with an adjuvant, in both
 CC precursor and post- translationally modified forms, and may be used to

CC generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
 CC marker for oesophageal cancer, and can be utilised as a marker for the
 CC targeted delivery of therapeutic agents to oesophageal cancer cells. It
 CC can also be used to generate diagnostic or therapeutic agents
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGPGGAPR 20
 |||||
 Db 43 RGRGAGAAARASGPGGAPR 62

RESULT 9
 AAB69946
 ID AAB69946 standard; protein; 180 AA.

AC AAB69946;

XX 27-APR-2001 (first entry)

XX Human NY-ESO-1 protein.

XX Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.

XX Homo sapiens.

XX WO200107917-A1.

XX 01-FEB-2001.

XX 14-JUL-2000; 2000WO-US019220.

XX 23-JUL-1999; 99US-00359503.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PA (CORR) CORNELL RES FOUND INC.

XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;

XX WPI; 2001-182822/18.

XX N-PSDB; AAF58634.

XX Method useful for determining the status (e.g. progression, regression or
 PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.

XX Example 5; Fig 3; 50pp; English.

XX The present sequence is human NY-ESO-1 protein. It is provided in a
 CC specification relating to a method for determining the status of a
 CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
 CC The method comprises assaying a sample taken from the patient for
 CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
 CC obtained to a prior value obtained from assay of a prior sample taken
 CC from the patient. Any difference between the values is indicative of a
 CC change in status of the cancerous condition. The method is useful for
 CC determining whether a cancerous condition is progressing, regressing or
 CC remaining stable, in particular in patients receiving treatment for a
 CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
 CC carcinoma

XX Sequence 180 AA;

Query Match 100.0%; Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGRGAGAAARASGPGGAPR 20
 |||||
 Db 43 RGRGAGAAARASGPGGAPR 62

RESULT 10
 AAG67164
 ID AAG67164 standard; protein; 180 AA.

XX AAG67164;

XX 13-NOV-2001 (first entry)

XX Amino acid sequence of cancer testis tumour antigen NY-ESO-1.

XX Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
 KW HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
 KW cancer; testis tumour.

XX Homo sapiens.

XX WO200162917-A1.

XX 30-AUG-2001.

XX 22-JAN-2001; 2001WO-US002126.

XX 22-FEB-2000; 2000US-00510635.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Lethe B, Boon-Falleur T;

XX WPI; 2001-550091/61.

DR N-PSDB; AAH75118.

XX Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
 PT for diagnosing testicular tumors.

XX Example 5; Fig 3; 50pp; English.

XX The present sequence represents cancer testis tumour antigen NY-ESO-1
 CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
 CC least one human leukocyte antigen (HLA) binding peptide, which binds to
 CC Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
 CC expressed in tumour mRNA and in testis, but not normal colon, kidney,
 CC liver or brain tissue. The presence or level of expression of NY-ESO-1
 CC may be assayed for the diagnosis of cancer, especially testis tumours

XX Sequence 180 AA;

Query Match 100.0%; Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGPGGAPR 20
 |||||
 Db 43 RGRGAGAAARASGPGGAPR 62

RESULT 11
 AAU01535
 ID AAU01535 standard; protein; 180 AA.

XX AAU01535;

XX 18-JUL-2001 (first entry)

XX Human NY-ESO-1 tumour rejection antigen precursor protein.

XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;

KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Modified-site 7
 FT /note= "Myristoylated"
 FT Modified-site 9
 FT /note= "Myristoylated"
 FT Modified-site 11
 FT /note= "Phosphorylated"
 FT Modified-site 98
 FT /note= "Phosphorylated"
 FT Modified-site 134
 FT /note= "Phosphorylated"
 FT Modified-site 138
 FT /note= "Phosphorylated"

XX WO200123560-A2.

XX 05-APR-2001.

XX 26-SEP-2000; 2000WO-US026411.

XX 29-SEP-1999; 99US-00408036.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Tureci O, Sahin U, Pfreundschuh M;

XX WPI; 2001-266156/27.

DR N-PSDB; AAS02254.

XX Polypeptides binding to major histocompatibility complex class II human
 FT leukocyte antigen-determining region molecule having amino acid sequence
 FT found in tumor rejection antigen precursor used for stimulating
 FT proliferation of helper T cells.

XX Claim 4; Fig 3; 62pp; English.

CC The sequence represents a human NY-ESO-1 tumour rejection antigen
 CC precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
 CC major histocompatibility complex (MHC) Class II molecules such as human
 CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
 CC proliferation of helper T cells. The peptides can be administered to an
 CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
 CC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
 CC or present in free form is useful for this stimulation. The nucleic acid
 CC is useful for screening for a cancerous condition, which involves
 CC contacting a subject sample to a cell line transfected with the
 CC immunoreactive cell (helper T cell), where interaction is indicative of
 CC cancer. In addition, a sample from a patient (for example, a body fluid
 CC or tissue) can be monitored for the amount of the complex present in the
 CC bloodstream. This is useful for determining regression, progression or
 CC onset of a cancerous condition. The method involves contacting the sample
 CC with a radioactive labelled or enzyme labelled monoclonal antibody which
 CC specifically binds with the complex

XX Sequence 180 AA;

Query Match 100.0%; Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPARGAARASGPGGAPR 20
 |||||
 Db 43 RGPARGAARASGPGGAPR 62

RESULT 12

AAE07714
 ID AAE07714 standard; protein; 180 AA.
 XX AC AAE07714;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human NY ESO-1 protein.
 XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 45..47
 FT /note= "Encoded by CCCGGGCGC"

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

DR N-PSDB; AAD14179, AAD14180.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.

XX Example 1; Fig 1; 134pp; English.

CC The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC protein

XX Sequence 180 AA;

Query Match 100.0%; Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPARGAARASGPGGAPR 20
 |||||
 Db 43 RGPARGAARASGPGGAPR 62

RESULT 13

AAU84818	
ID	AAU84818 standard; protein; 180 AA.
XX	
AC	AAU84818;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Human NYN501a consensus sequence.
XX	
KW	Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW	viral infection; human immunodeficiency virus; melanoma;
KW	bacterial infection; Salmonella; Legionella; parasitic infection;
KW	Trypanosoma; Toxoplasma; Giardia.
XX	
OS	Homo sapiens.
XX	
PN	WO200190197-A1.
XX	
PD	29-NOV-2001.
XX	
PF	25-MAY-2001; 2001WO-AU000622.
XX	
PR	26-MAY-2000; 2000AU-00007761.
XX	
PA	(AUSU) UNIV AUSTRALIAN NAT.
XX	
PI	Thomson SA, Ramshaw IA;
XX	
DR	WPI; 2002-147575/19.
XX	
PT	New synthetic polypeptides having several different segments of at least
PT	one parent polypeptide linked together differently compared to the
PT	linkage in the parent polypeptide, for inducing immune response against a
PT	pathogen or cancer.
XX	
PS	Example 3; Fig 27; 364pp; English.
XX	
CC	The invention relates to a new synthetic polypeptide (I) comprising
CC	several different segments of at least one parent polypeptide linked
CC	together in a different relationship relative to their linkage in the
CC	parent polypeptide to impede, abrogate or otherwise alter at least one
CC	function associated with the parent polypeptide and for inducing an
CC	immune response against a pathogen or cancer. Also included are a
CC	synthetic polynucleotide encoding and a computer system for designing the
CC	synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC	are referred to as a Savine. The synthetic polypeptide is useful for
CC	modulating immune responses preferably directed against a pathogen or a
CC	cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC	and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC	oesophagus, brain, testicle, uterus), as potentiating agents.
CC	Compositions comprising the polypeptide may be used in the treatment or
CC	prophylaxis against viral (such as infections caused by HIV (human
CC	immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC	virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC	(e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC	Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC	(e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC	Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC	a consensus sequence for a parent protein used to design a savine of the
CC	invention
XX	
SQ	Sequence 180 AA;
Query Match 100.0%; Score 107; DB 5; Length 180;	
Best Local Similarity 100.0%; Pred. No. 7.3e-05;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 RGPRGAGAAASGPGGAPR 20
Db	43 RGPRGAGAAASGPGGAPR 62
RESULT 14	

AAU11543	
ID	AAU11543 standard; protein; 180 AA.
XX	
AC	AAU11543;
XX	
DT	12-MAR-2002 (first entry)
XX	
DE	Human tumour associated antigen NY-ESO.
XX	
KW	Human; tumour associated antigen; NY-ESO; human leukocyte antigen;
KW	major histocompatibility complex; MHC; HLA-A2.2; vaccine; cancer; HIV;
KW	human immunodeficiency virus infection; cytostatic; virucide;
KW	housekeeping epitope; adoptive immunotherapy; neoplastic disease;
KW	viral disease; hepatitis virus; papilloma virus; tumour; leukaemia;
KW	lymphoma; breast cancer; prostate cancer; lung cancer;
KW	parasitic infection; Chlamydia; Trypanosoma; Toxoplasma.
XX	
OS	Homo sapiens.
XX	
PN	WO200182963-A2.
XX	
PD	08-NOV-2001.
XX	
PF	27-APR-2001; 2001WO-US013806.
XX	
PR	28-APR-2000; 2000US-00560465.
PR	28-APR-2000; 2000US-00561074.
PR	28-APR-2000; 2000US-00561571.
PR	28-APR-2000; 2000US-00561572.
XX	
PA	(CTLI-) CTL IMMUNOTHERAPIES CORP.
XX	
PI	Simard JLL, Diamond DC, Lei X;
XX	
DR	WPI; 2002-066492/09.
XX	
PT	Novel vaccine useful for treating neoplastic and viral diseases,
PT	comprises a first housekeeping epitope derived from a first antigen
PT	associated with a first target cell.
XX	
XX	Example 23; Fig 17; 131pp; English.
XX	
CC	The invention relates to a vaccine comprising a first housekeeping
CC	epitope derived from a first antigen associated with a first target cell.
CC	Also included are an isolated T cell expressing a T cell receptor
CC	specific for a major histocompatibility complex (MHC)-peptide complex
CC	comprising a first housekeeping epitope which is derived from a first
CC	antigen associated with a first target cell, selecting an epitope (or
CC	peptide sequence) from a population of peptide fragments of an antigen
CC	associated with a target in a host, where the fragments have a known or
CC	predicted affinity for a MHC receptor peptide binding cleft of the host,
CC	where the epitope selected corresponds to a product of proteolytic
CC	cleavage of the antigen in a cell of the host and a nucleic acid
CC	construct comprising a first coding region, where the first coding region
CC	comprises a first sequence encoding at least a first housekeeping epitope derived from
CC	the first polypeptide comprising a first target cell; the epitopes,
CC	a first antigen associated with a first target cell; the epitopes,
CC	peptides, vaccines and nucleic acids are useful in the manufacture of a
CC	medicament for use in adoptive immunotherapy and for prevention and
CC	treatment of neoplastic and viral diseases (e.g. human immunodeficiency
CC	virus, HIV, infection, hepatitis virus and papilloma virus), cancers
CC	(e.g. tumours, leukaemia, lymphoma, breast cancer, prostate cancer and
CC	lung cancer), infection of cells by intracellular parasites (e.g.
CC	Chlamydia, Trypanosoma and toxoplasma) and many other examples given in
CC	the specification. The invention permits the vaccine designer to ignore
CC	peptides that, despite predicted high binding affinity for MHC, will
CC	never be useful because they cannot be presented by target cells. The
CC	invention provides a major advance in vaccine design, one that combines
CC	the power of antigen sequence analysis with the fundamental realities of
CC	immunology. The invention allows for the simple and effective selection
CC	of meaningful epitopes for creation of MHC class I or class II vaccines
CC	using any polypeptide sequence corresponding to a desired target. The
CC	present sequence is an HLA-A2.1 (human leukocyte antigen) presenting

CC target cell protein from which epitopes of the invention may be derived,
CC NY-ESO (a tumour associated antigen)
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPRGAGAAASGPGGAPR 20
|||||
Db 43 RGPRGAGAAASGPGGAPR 62

RESULT 15

ABR58672

ID ABR58672 standard; protein; 180 AA.

XX

AC ABR58672;

XX

DT 09-JUL-2003 (first entry)

XX

XX Human cancer related protein SEQ ID NO:329.

DE

XX

XX

KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;

KW heart disease; atherosclerosis; endometriosis.

XX

OS Homo sapiens.

XX

XX WO2003025139-A2.

PN

XX

PD 27-MAR-2003.

XX

XX

PF 17-SEP-2002; 2002WO-US029560.

XX

PR 17-SEP-2001; 2001US-0323469P.

PR 20-SEP-2001; 2001US-0323887P.

PR 13-NOV-2001; 2001US-0350666P.

PR 08-FEB-2002; 2002US-0355145P.

PR 08-FEB-2002; 2002US-0355257P.

PR 12-APR-2002; 2002US-0372246P.

XX

XX (EOSB-) EOS BIOTECHNOLOGY INC.

PA

XX

PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;

PI Zlotnik A;

XX

DR WPI; 2003-354600/33.

DR N-PSDB; ACC72823.

XX

XX

PT New genes that are up-regulated or down-regulated in cancers, useful as

PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as

PT therapeutic targets for screening drugs for treating these diseases.

XX

PS Claim 12; Page 757-758; 767pp; English.

XX

CC The present invention describes an isolated nucleic acid molecule, which

CC comprises the sequence of any of the genes that are up-regulated or down-

CC regulated in specific cancers (e.g. about 1031 genes up-regulated in

CC acute lymphocytic leukemia). ACC72841 to ACC72860 represent cancer

CC related gene nucleotide sequences which encode the proteins given in

CC ABR58521 to ABR58709. Also described: (1) determining the presence or

CC absence of a pathological cell in a patient; (2) an expression vector

CC comprising a nucleic acid molecule described above; (3) a host cell

CC comprising the vector; (4) an isolated polypeptide, which is encoded by

CC the nucleic acid; (5) an antibody that specifically binds the polypeptide

CC of (4); (6) specifically targeting a compound to a pathological cell in a

CC patient by administering to the patient the antibody above; and (7) a

CC drug screening assay. The nucleic acid is useful as diagnostic markers or

CC therapeutic targets. In particular, the nucleic acid is useful for

CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,

CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,

CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,

CC atherosclerosis and endometriosis. The nucleic acid is also useful in

CC drug screening, particularly for identifying agents for treating these

CC pathologies

XX

SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 6; Length 180;

Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPRGAGAAASGPGGAPR 20

|||||

Db 43 RGPRGAGAAASGPGGAPR 62

Search completed: September 11, 2005, 01:38:04

Job time : 28.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:28:54 ; Search time 5.61905 Seconds
(without alignments)
342.466 Million cell updates/sec

Title: US-09-529-206E-4_COPY_43_62
Perfect score: 107
Sequence: 1 RGRGAGARASGPGGAPR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	62.6	627	2 T35608	polyketide hydroxy
2	60	56.1	893	2 S51603	receptor-like tyro
3	60	56.1	981	2 S51604	receptor-like tyro
4	60	56.1	1005	2 S49015	receptor tyrosine
5	59	55.1	129	1 OTHU5B	cytochrome-c oxida
6	59	55.1	877	2 I48967	brain-specific kin
7	58.5	54.7	566	2 T21096	hypothetical prote
8	58.5	54.7	692	2 T21095	hypothetical prote
9	57	53.3	129	1 JC2254	cytochrome-c oxida
10	57	53.3	355	2 T36273	hypothetical prote
11	56	52.3	331	2 S78452	POU-domain protein
12	55	51.4	201	2 C40040	alternative splici
13	55	51.4	201	2 S26404	alternative splici
14	55	51.4	248	2 A40040	alternative splici
15	55	51.4	250	2 T46417	hypothetical prote
16	55	51.4	222	2 B40040	alternative splici
17	55	51.4	1215	2 T32734	myosin-IA - Acanth
18	54.5	50.9	496	2 F83124	hypothetical prote
19	54	50.5	388	2 T29173	probable transcrip
20	54	50.5	597	2 S51212	BAK5 protein - bov
21	54	50.5	730	2 A36226	collagen alpha 1 c
22	54	50.5	1733	1 B45344	probable nuclear a
23	53.5	50.0	627	2 A44112	spidroin 2, dragli
24	53.5	50.0	3190	2 T13828	CREB-binding prote
25	53	49.5	485	1 F71275	probable periplasm
26	53	49.5	1306	2 A70934	hypothetical glyci
27	52.5	49.1	450	2 A34169	alpha-2A-adrenergi
28	52.5	49.1	782	2 S33945	late protein, 100K
29	52.5	49.1	1690	2 T35694	ATP dependent DNA

30 52.5 49.1 1737 2 T00209 MEGF8 protein - hu
31 52 48.6 295 2 T04483 probable ring fing
32 52 48.6 314 2 JC5273 paired type homeob
33 52 48.6 373 2 A47234 homeobox protein H
34 52 48.6 676 1 EDBE22 immediate-early pr
35 52 48.6 676 1 EDBE23 immediate-early pr
36 52 48.6 1171 2 T42372 probable guanylate
37 52 48.6 1256 2 JE0209 brain-specific ang
38 52 48.6 1487 1 EDBE11 immediate-early pr
39 52 48.6 1487 1 EDBE11 immediate-early pr
40 51.5 48.1 1958 2 B40505 155K transcripion
41 51 47.7 198 2 AS7717 hypothetcal prote
42 51 47.7 327 2 T47231 transcrption fact
43 51 47.7 420 2 IS9234 fibrillarlin [impor
44 51 47.7 632 2 S42731 octamer binding tr
45 51 47.7 688 2 T48796 collagen alpha 1 c
probable ATP-depen

ALIGNMENTS

RESULT 1

T35608 polyketide hydroxylase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35608
R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21584
A;Accession: T35608
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-627 <SEE>
A;Cross-references: UNIPROT:P42534; EMBL:AL079356; PIDN:CAB45603.1; GSPDB:GN000070; SCORE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC6G9.12c
C;Superfamily: tetracycline 6-hydroxylase

Query Match 62.6%; Score 67; DB 2; Length 627;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GPRGAGARASGPGGG 17
|||
Db 447 GPRGAGAPGGGPGGG 462

RESULT 2

S51603 receptor-like tyrosine kinase Etk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S51603
R;Maisompierre, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fa
A;Reference number: S49015; MUID:94067777; PMID:7504232
A;Accession: S51603
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-893 <MAI>
A;Cross-references: UNIPROT:P54757; EMBL:S68028
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C;Keywords: ATP; transmembrane protein
F;563-829/Domain: protein kinase homology <KIN>
F;571-579/Region: protein kinase ATP-binding motif

Query Match 56.1%; Score 60; DB 2; Length 893;
Best Local Similarity 61.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGAAASGPGGG--APR 20
||||| | | | |
Db 5 GPRGAGRRRTQGRGGGDTPT 25

RESULT 3
S51604
A;Title: receptor-like tyrosine kinase Etk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C;Accession: S51604
R;Maisonpierrre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A;Reference number: S49015; MUID:9406777; PMID:7504232
A;Accession: S51604
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-981 <MAI>
A;Cross-references: EMBL:S68029
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C;Keywords: ATP; transmembrane protein
F;651-917/Domain: protein kinase homology <KIN>
F;659-667/Region: protein kinase ATP-binding motif

Query Match 56.1%; Score 60; DB 2; Length 981;
Best Local Similarity 61.9%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGAAASGPGGG--APR 20
||||| | | | |
Db 5 GPRGAGRRRTQGRGGGDTPT 25

RESULT 4
S49015
A;Title: receptor tyrosine kinase Etk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S49015; S51602
R;Maisonpierrre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A;Reference number: S49015; MUID:9406777; PMID:7504232
A;Accession: S49015
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1005 <MAI>
A;Cross-references: UNIPROT:P54757; EMBL:S68024
A;Note: the authors translated the codon GAC for residue 170 as Glu
A;Accession: S51602
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305, 'G', 359-1005 <MA2>
A;Cross-references: EMBL:S68026
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C;Keywords: ATP; transmembrane protein
F;675-941/Domain: protein kinase homology <KIN>
F;683-691/Region: protein kinase ATP-binding motif

Query Match 56.1%; Score 60; DB 2; Length 1005;
Best Local Similarity 61.9%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGAAASGPGGG--APR 20
||||| | | | |
Db 5 GPRGAGRRRTQGRGGGDTPT 25

RESULT 5

OTHUSB
cytochrome-c oxidase (EC 1.9.3.1) chain Vb precursor - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: J0324; A39063; S74198; A28817
R;Zeviani, M.; Sakoda, S.; Sherbany, A.A.; Nakase, H.; Rizzuto, R.; Samitt, C.E.; DiMauro
Gene 65, 1-11, 1988
A;Title: Sequence of cDNAs encoding subunit Vb of human and bovine cytochrome c oxidase
A;Reference number: J0324; MUID:88284368; PMID:2840351
A;Accession: J0324
A;Molecule type: mRNA
A;Residues: 1-129 <ZEV>
A;Cross-references: UNIPROT:P10606; UNIPROT:Q99610; EMBL:M19961; NID:G180940; PIDN:AAA5
R;Lomax, M.I.; Hsieh, C.L.; Darvas, B.T.; Francke, U.
Genomics 10, 1-9, 1991
A;Title: Structure of the human cytochrome c oxidase subunit Vb gene and chromosomal ma
A;Reference number: A39063; MUID:91257815; PMID:1646156
A;Accession: A39063
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108, 'E', 110-129 <LOM>
A;Cross-references: EMBL:M59250
A;Note: the authors translated the codon GGC for residue 21 as His
R;Bachman, N.J.; Yang, T.L.; Dasen, J.S.; Ernst, R.E.; Lomax, M.I.
Arch. Biochem. Biophys. 333, 152-162, 1996
A;Title: Phylogenetic footprinting of the human cytochrome c oxidase subunit Vb promote
A;Reference number: S74198; MUID:96400390; PMID:8806766
A;Accession: S74198
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-35, 'TR' <BAC>
A;Cross-references: EMBL:U41284; NID:G1679627; PIDN:AAB19185.1; PID:G1679628
C;Genetics:
A;Gene: GDB:COX5B
A;Cross-references: GDB:127530; OMIM:123866
A;Map position: 2cen-2q13
A;Genome: nuclear
C;Complex: part of a 13 chain complex spanning the inner mitochondrial membrane and con
(see PIR:OTHUSA), Vb, V1a (see PIR:OGHU6A), V1b (see PIR:OGHU6B), V1c (see PIR:OGHU6C)
m dimers within the mitochondrial inner-membrane
C;Function:
A;Description: the cytochrome-c oxidase complex catalyzes the oxidation of four molecu
ns from the mitochondrial matrix producing two molecules of water and lowering the conc
A;Note: the role of chain Vb is not clear
C;Superfamily: mammalian cytochrome-c oxidase chain Vb
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membran
F;1-31/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;32-129/Product: cytochrome-c oxidase chain Vb #status predicted <MAT>
F;91,93,113,116/Binding site: zinc (Cys) #status predicted

Query Match 55.1%; Score 59; DB 1; Length 129;
Best Local Similarity 57.9%; Pred. No. 4;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RGPFGAGAAASGPGGGAP 19
||| | | | | | | | | | | | | |
Db 20 RGPFGAAAMRSMASGGGVP 38

RESULT 6
I48967
brain-specific kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48967
R;Zhou, R.R.; Copeland, T.D.; Kromer, L.F.; Schulz, N.T.
J. Neurosci. Res. 37, 129-143, 1994
A;Title: Isolation and characterization of Bsk, a growth factor receptor-like tyrosine
A;Reference number: I48967; MUID:94194581; PMID:8145300
A;Accession: I48967
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-877 <RES>

A;Cross-references: UNIPROT:Q60629; EMBL:U07357; NID:9466369; PIDN:AAAL7038.1; PID:94663
C;Gene: Bsk
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C;Keywords: ATP; transmembrane protein
F;512-778/Domain: protein kinase homology <XIN>
F;520-528/Region: protein kinase ATP-binding motif
F;801-868/Domain: SAM homology <SAM>

Query Match 55.1%; Score 59; DB 2; Length 877;
Best Local Similarity 61.9%; Pred. No. 22;
Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGARASGPGG--APR 20
Db 5 GPRGAGHRRQTGGGGDTPR 25
||||| | | | | |

RESULT 7
T21096
hypothetical protein F18H3.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21096
R;Coles, L.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19373
A;Accession: T21096
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-566 <WIL>
A;Cross-references: UNIPROT:Q19581; EMBL:Z50110; PIDN:CAA90446.1; GSPDB:GN000028; CESP:FI
A;Experimental source: clone F18H3
C;Genetics:
A;Gene: CESP:F18H3.3b
A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match 54.7%; Score 58.5; DB 2; Length 566;
Best Local Similarity 65.0%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 3 PRGAGARASGPG---GGAP 19
Db 530 PRPAGAPRVGGPGVQMGAP 549
||| | | | | |

RESULT 8
T21095
hypothetical protein F18H3.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21095
R;Coles, L.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19373
A;Accession: T21095
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-692 <WIL>
A;Cross-references: UNIPROT:Q19579; EMBL:Z50110; PIDN:CAA90444.1; GSPDB:GN000028; CESP:FI
A;Experimental source: clone F18H3
C;Genetics:
A;Gene: CESP:F18H3.3a
A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match 54.7%; Score 58.5; DB 2; Length 692;
Best Local Similarity 65.0%; Pred. No. 21;
Matches 13; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 3 PRGAGARASGPG---GGAP 19
Db 530 PRPAGAPRVGGPGVQMGAP 549
||| | | | | |

RESULT 9
JC2254
cytochrome-c oxidase (EC 1.9.3.1) chain Vb precursor - rat
N;Alternate names: cytochrome-c oxidase (EC 1.9.3.1) chain V1a*
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JC2254; J02255; S05318; S65375
R;Hoshinaga, H.; Amuro, N.; Goto, Y.; Okazaki, T.
J. Biochem. 115, 194-201, 1994
A;Title: Molecular cloning and characterization of the rat cytochrome c oxidase subunit
A;Reference number: JC2254; MUID:94266742; PMID:8206867
A;Accession: JC2254
A;Molecule type: mRNA
A;Residues: 1-129 <HOS>
A;Cross-references: UNIPROT:P12075; DDBJ:D10952; NID:9493694; PIDN:BAA01744.1; PID:9493
A;Experimental source: liver
A;Accession: JC2255
A;Molecule type: DNA
A;Residues: 1-129 <HO2>
A;Cross-references: DDBJ:D10951
A;Experimental source: lambda COXVb741
R;Goto, Y.; Amuro, N.; Okazaki, T.
Nucleic Acids Res. 17, 6389, 1989
A;Title: Nucleotide sequence of cDNA for rat liver and brain cytochrome c oxidase subun
A;Reference number: S05318; MUID:89366688; PMID:2549512
A;Accession: S05318
A;Molecule type: mRNA
A;Residues: 31-129 <GOT>
A;Cross-references: EMBL:X14208
R;Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-ter.
A;Reference number: S65372; MUID:95324529; PMID:7601105
A;Accession: S65375
A;Molecule type: protein
A;Residues: 32-41 <SCH>
A;Experimental source: liver
C;Genetics:
A;Gene: COXVb-1
A;Introns: 35/1; 59/3; 93/1
A;Note: intronless gene COXVb-2 apparently a nonfunctional processed pseudogene
C;Superfamily: mammalian cytochrome-c oxidase chain Vb
C;Keywords: membrane-associated complex; mitochondrial inner membrane; mitochondrion; o
F;1-31/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;32-129/Product: cytochrome-c oxidase chain Vb #status predicted <MAT>

Query Match 53.3%; Score 57; DB 1; Length 129;
Best Local Similarity 55.6%; Pred. No. 8.2;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GPRGAGARASGPGGAP 19
Db 21 GPRGVAATRSASGGGVP 38
||| | | | | |

RESULT 10
T36273
hypothetical protein SCE68.23c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36273
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21576
A;Accession: T36273
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-355 <MUR>

T46417
hypothetical protein DKFZp434K1323.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46417
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: 223034
A;Accession: T46417
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-250 <AAA>
A;Cross-references: UNIPROT:Q9NSV7; EMBL:AL137714
A;Experimental source: adult testis; clone DKFZp434K1323
C;Genetics:
A;Note: DKFZp434K1323.1

Query Match 51.4%; Score 55; DB 2; Length 250;
Best Local Similarity 68.8%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RGRGAGAAARASGPGG 16
||| ||| ||| ||| |||
Db 9 RGRGGGGRRAALGPGG 24

Search completed: September 11, 2005, 01:43:53
Job time : 6.61905 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:20:48 ; Search time 26.4762 Seconds
(without alignments)
386.822 Million cell updates/sec

Title: US-09-529-206E-4_COPY_43_62
Perfect score: 107
Sequence: 1 RGRGAGARASGPGGAPR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	142	2 Q9NY13	Q9ny13 homo sapien
2	107	100.0	180	1 CTG1_HUMAN	P78358 homo sapien
3	99	92.5	210	1 CTG2_HUMAN	O75638 homo sapien
4	67	62.6	627	1 HYDL_STRCO	P42534 streptomyc
5	64	59.8	337	1 CT86_HUMAN	Q9bz19 homo sapien
6	62	57.9	301	2 Q8WSZ3	Q8wsz3 nephila cla
7	62	57.9	550	2 Q86P11	Q86p11 toxoplasma
8	62	57.9	1039	2 Q8S0W4	Q8s0w4 oryza sativ
9	62	57.9	1039	2 Q6F2Y0	Q6f2y0 oryza sativ
10	61.5	57.5	1953	2 Q9BI77	Q9bi77 nephila ina
11	60	56.1	450	1 A2AA_HUMAN	P08913 homo sapien
12	60	56.1	721	1 PUB2_RAT	Q99pf5 rattus norv
13	60	56.1	926	1 CEZ2_MOUSE	Q8r554 mus musculu
14	60	56.1	1005	1 EPAS_RAT	P54757 rattus norv
15	59	55.1	129	1 COXB_HUMAN	P10606 homo sapien
16	59	55.1	129	2 Q6FHJ9	Q6fhj9 homo sapien
17	59	55.1	129	2 Q6FH44	Q6fhm4 homo sapien
18	59	55.1	420	2 Q8CBY9	Q8cb9 mus musculu
19	59	55.1	538	2 Q8C278	Q8c278 mus musculu
20	59	55.1	681	2 Q8C276	Q8c276 mus musculu
21	59	55.1	819	2 Q6PFV6	Q6pfv6 mus musculu
22	59	55.1	877	1 EPAS_MOUSE	Q60629 mus musculu
23	58.5	54.7	563	2 Q9BIT5	Q9bit5 nephila ina
24	58.5	54.7	566	2 Q195B1	Q195b1 caenorhabdi
25	58.5	54.7	692	2 Q19579	Q19579 caenorhabdi
26	58	54.2	775	2 Q9F342	Q9f342 streptomyc
27	57	53.3	129	1 COXB_RAT	P12075 rattus norv
28	57	53.3	129	2 Q9D8E1	Q9d8e1 mus musculu
29	57	53.3	329	2 Q6NLK4	Q6nlk4 drosophila
30	57	53.3	355	2 Q9WX09	Q9wx09 streptomyc
31	57	53.3	412	2 Q960D3	Q960d3 drosophila

32 57 53.3 437 2 Q8KUG4
33 57 53.3 443 2 Q9VBX3
34 57 53.3 457 2 Q94LK1
35 57 53.3 457 2 Q7G604
36 57 53.3 644 2 Q688J5
37 57 53.3 853 2 Q8VQZ0
38 57 53.3 857 2 Q85783
39 57 53.3 866 1 SRC2_HUMAN
40 56 52.3 114 2 Q6B461
41 56 52.3 158 2 Q8C2G2
42 56 52.3 200 2 Q8W3A2
43 56 52.3 256 2 Q96MK8
44 56 52.3 478 2 Q82F52
45 56 52.3 520 2 Q7XLL8

Q8kug4 actinosyne
Q9vbx3 drosophila
Q94lk1 oryza sativ
Q7g604 oryza sativ
Q688j5 oryza sativ
Q8vqz0 myxococcus
Q85783 myxococcus
Q96gp6 homo sapien
Q6b461 suid herpes
Q8c2g2 mus musculu
Q8w3a2 oryza sativ
Q96mk8 homo sapien
Q82f52 streptomyc
Q7xll8 oryza sativ

RESULT 1

Q9NY13 PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DB Hypothetical protein LAGE-2 (Fragment).
GN Names=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275978; CAB76945.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 107; DB 2; Length 142;

Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGARASGPGGAPR 20

|||||
DB 17 RGRGAGARASGPGGAPR 36

RESULT 2

CTG1_HUMAN STANDARD; PRT; 180 AA.
ID CTG1_HUMAN
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).
DE ESO-1).
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
Chen Y.-T., Scanlan M.J., Sahin U., Tuerci O., Gure A.O., Tsang S.,
Williamson B., Stockert B., Pfleundschuh M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected
by autologous antibody screening.";
Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918 (1997).
RN [2]

Query Match 92.5%; Score 99; DB 1; Length 210;
 Best Local Similarity 95.0%; Pred. No. 0.0032;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGRPGAGNARASGPGGAPR 20
 |||||
 DB 43 RGRPGAGNARASGPGGAPR 62

RESULT 4
 HYDL_STRCO STANDARD; PRT; 627 AA.
 AC P42534; Q9S2L7;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Putative polyketide hydroxylase (EC 1.14.13.-) (Whie ORF VIII).
 GN OrderedLocusNames=SC05321; ORFNames=SC6G9.12c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris K.D., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 RN [2]
 RP SEQUENCE OF 1-255 FROM N.A.
 RC STRAIN=A3(2).
 RX MEDLINE=94075247; PubMed=8253693;
 RA Blanco G., Pereda A., Brian P., Mendez C., Chater K.F., Salas J.A.;
 RT "A hydroxylase-like gene product contributes to synthesis of a
 RT polyketide spore pigment in Streptomyces halstedii.";
 RL J. Bacteriol. 175:8043-8048(1993)
 CC -1- FUNCTION: Involved in developmentally regulated synthesis of a
 CC compound biosynthetically related to polyketide antibiotics which
 CC is essential for spore color in Streptococcus coelicolor.
 CC -1- COPACTOR: FAD (By similarity).
 CC -1- SIMILARITY: Belongs to the pheA/tfDB FAD monooxygenase family.
 CC
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 CC
 CC -----
 CC EMBL; AL3919123; CAB45603.1; -.
 CC EMBL; X74213; CAAS2289.1; -.
 CC PIR; T35608; T35608.
 CC InterPro; IPR008160; Collagen.
 CC InterPro; IPR000733; Flav_monooxygenase.
 CC InterPro; IPR002938; MoxF_FAD binding.
 CC InterPro; IPR003042; Rng_monooxygenase.
 CC Pfam; PF01494; Rng binding 3; 1.
 CC Pfam; PF01360; Monooxygenase; 1.
 CC PRINTS; PR00420; RNMNOXGNASE.
 CC Complete proteome; FAD; Flavoprotein; Oxidoreductase.
 NP_BIND 22 51 FAD (Potential).
 DR EMBL; AL354776; CAC17565.2; -.
 DR HSSP; P42771; 2A5E.
 DR Genew; HGNC:16217; C20orf86.
 DR InterPro; IPR002110; ANK.

FT NP_BIND 309 319 FAD (Potential).
 FT CONFLICT 60 60 R -> A (in Ref. 2).
 FT CONFLICT 145 145 L -> LH (in Ref. 2).
 FT CONFLICT 234 234 C -> S (in Ref. 2).
 SQ SEQUENCE 627 AA; 64557 MW; 746B84A2A9E951C CRC64;

Query Match 62.6%; Score 67; DB 1; Length 627;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GPRGAGNARASGPGGG 17
 |||||
 DB 447 GPRGAGNARASGPGGG 462

RESULT 5
 CT86_HUMAN STANDARD; PRT; 337 AA.
 AC Q9B219;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical protein c20orf86.
 GN Name=C20orf86;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.P., Bates K.N., Bead L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharvaisho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Pratchinagam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -1- SIMILARITY: Contains 2 ANK repeats.
 CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
 CC
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 CC
 CC -----
 CC EMBL; AL354776; CAC17565.2; -.
 CC HSSP; P42771; 2A5E.
 CC Genew; HGNC:16217; C20orf86.
 CC InterPro; IPR002110; ANK.

```

DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00023; Ank; 3.
DR PRINTS; PRO1415; ANKYRIN.
DR SMART; SM00248; Ank; 2.
DR PROSITE; PS0297; ANK_REPEAT; 1.
DR PROSITE; PS00088; ANK_REPEAT; 2.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PS00053; UBIQUITIN_2; 1.
DR ANK repeat; Hypothetical protein; Polymorphism; Repeat.
FT DOMAIN 88 164 Ubiquitin-like.
FT REPEAT 211 241 ANK 1.
FT REPEAT 244 273 ANK 2.
FT VARIANT 287 287
FT SEQUENCE 337 AA; 36714 MW; EC8BA4AD414756CB CRC64;
Query Match 59.8%; Score 64; DB 1; Length 337;
Best Local Similarity 65.0%; Pred. No. 26;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGRGAGAGARASGPGGAPR 20
| | | | | | | | | | | | | | | |
Db 3 RAAAGAGGARAAGTGGASR 22
| | | | | | | | | | | | | | | |

RESULT 6
Q8WSZ3 PRELIMINARY; PRT; 301 AA.
AC Q8WSZ3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Dragline silk protein spidroin 2 (Fragment).
OS Nephila clavata (Joro spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneidae; Tetragnathidae; Nephila.
OX NCBI_TaxID=70342;
RN [1]
RP SEQUENCE FROM N.A.
RA Ma H.W., Zhang L.S., Lu Y.M., Liu Z.S., Zhang Y.J.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF441245; AAL32472.1; -.
FT NON_TER 1 1
FT NON_TER 301 301
FT SEQUENCE 301 AA; 25396 MW; 8C69428B5684ED74 CRC64;
Query Match 57.9%; Score 62; DB 2; Length 301;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GPRGAGARASGPGGAP 19
| | | | | | | | | | | | | | | |
Db 130 GPGGAAAAAAGPGGYG 147
| | | | | | | | | | | | | | | |

RESULT 7
Q86P11 PRELIMINARY; PRT; 550 AA.
AC Q86P11;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Jip2.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
RA Jiang L., Shu H., Luo S., Wu X., Cai L., Wang D., Zeng Q.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY208675; AAO43429.1; -.

SQ SEQUENCE 550 AA; 57890 MW; 18C71B4974BF0F34 CRC64;
Query Match 57.9%; Score 62; DB 2; Length 550;
Best Local Similarity 63.2%; Pred. No. 65;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GPRGAGARASGPGGAPR 20
| | | | | | | | | | | | | | | |
Db 524 GPGAGAAQADGIGAGGPR 542
| | | | | | | | | | | | | | | |

RESULT 8
Q8SOW4 PRELIMINARY; PRT; 1039 AA.
AC Q8SOW4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE QJ1014 G12.10 protein.
GN Name=QJ1014_G12.10;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa K., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagaaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara K., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003372; BAB89076.1; -.
DR Gramene; Q8SOW4; -.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR007228; DUF390.
DR InterPro; IPR007321; Transposase_28.
DR Pfam; PF04094; DUF390; 1.
DR Pfam; PF04195; Transposase_28; 1.
SQ SEQUENCE 1039 AA; 112082 MW; A9A60FD3487B5DFD CRC64;
Query Match 57.9%; Score 62; DB 2; Length 1039;
Best Local Similarity 73.7%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 3 PRGAGARASG--PGGAP 19
| | | | | | | | | | | | | | | |
Db 363 PRGGAGARASSRRPEGAP 381
| | | | | | | | | | | | | | | |

RESULT 9
Q6F2Y0 PRELIMINARY; PRT; 1039 AA.
AC Q6F2Y0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSJNBa0038E22.10.
GN Name=OSJNBa0038E22.10;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Ehrhartoidae; Oryzae; Oryza.
OX	NCBI_TaxID=39947;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Chow T.-Y., Heing Y.-I., Chen C.-S., Chen H.-H., Liu S.-M.,
RA	Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA	Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA	Hsiung J.-N., Hau C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
RA	Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA	Wu H.-P., Shaw J.-F., McCombie W.R., Spiegel L., de la Bastide M.,
RA	*Zutavern T., *Muller S., *Macnamara L.V., *Balijs V., Bell M.,
RA	*Willer B., *Katzenberger F., *Andrade M.V., *Dike S.,
RA	*O'Shaughnessy A., *Palmer L., *Dedhia N.;
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AC132484; AA73650.1; -
DR	InterPro; IPR011038; Calycin.
DR	InterPro; IPR007228; DUF390.
DR	InterPro; IPR007321; Transposase_28.
DR	Pfam; PF04094; DUF390; 1.
DR	Pfam; PF04195; Transposase_28; 1.
KW	Hypothetical protein.
QY	SEQUENCE 1039 AA; 111214 MW; 856219894B2FB717 CRC64;
Db	Query Match 57.9%; Score 62; DB 2; Length 1039;
	Best Local Similarity 73.7%; Pred. No. 1.e+02;
	Matches 14; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY	3 PRGGAARASG--PGGGAP 19
Db	
	322 PRGGAARASGRPEGAAP 340
RESULT 10	
QBIT7	PRELIMINARY; PRT; 1953 AA.
ID	QBIT7;
AC	QBIT7;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Major ampullate spiderin 2-like protein (Fragment).
OS	Nephila inaurata madagascariensis.
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC	Araconomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.
OX	NCBI_TaxID=115969;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=21179804; PubMed=11283372; DOI=10.1126/science.1057561;
RA	Gatesy J.E., Hayashi C., Motriuk D., Woods J., Lewis R.;
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF350276; AAK30605.1; -
FT	NON_TER 1 1
FT	NON_TER 1953 1953
FT	NON_TER 1953 1953
QY	SEQUENCE 1953 AA; 159383 MW; C82B4DACD043C3BD CRC64;
Db	Query Match 57.5%; Score 61.5; DB 2; Length 1953;
	Best Local Similarity 68.4%; Pred. No. 2.2e+02;
	Matches 13; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
QY	1 RGRPGAGARASPGGGAP 19
Db	: : :
	152 QGRPGCAA-AAGPGGYGP 169
RESULT 11	
A2AA_HUMAN	
ID	A2AA_HUMAN
STANDARD;	PRT; 450 AA.

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [9]
RP MUTAGENESIS OF PHE-412.
RX MEDLINE=9132079; PubMed=1678390;
RA Suryanarayana S., Daunt D.A., von Zastrow M., Kobilka B.K.;
RT "A point mutation in the seventh hydrophobic domain of the alpha 2
RT adrenergic receptor increases its affinity for a family of beta
RT receptor antagonists.";
RL J. Biol. Chem. 266:15488-15492 (1991).
RN [10]
RP MUTAGENESIS OF ASPARTIC ACID AND SERINE RESIDUES.
RX MEDLINE=9134259; PubMed=1678850;
RA Wang C.-D., Buck M.A., Fraser C.M.;
RT "Site-directed mutagenesis of alpha 2a-adrenergic receptors:
RT Identification of amino acids involved in ligand binding and receptor
RT activation by agonists.";
RL Mol. Pharmacol. 40:168-179 (1991).
CC -!- FUNCTION: Alpha-2 adrenergic receptors mediate the catecholamine-
CC induced inhibition of adenylate cyclase through the action of G
CC proteins. The rank order of potency for agonists of this receptor
CC is oxymetazoline > clonidine > epinephrine > norepinephrine >
CC phenylephrine > dopamine > p-synephrine > p-tyramine > serotonin =
CC p-octopamine. For antagonists, the rank order is yohimbine >
CC phentolamine = mianserin > chlorpromazine = spiperone = prazosin
CC > propranolol > alprenolol = pindolol.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC
CC EMBL; M23533; AAA51665.1; -.
CC EMBL; M18415; AAA51664.1; -.
CC EMBL; AF262016; AAG00447.2; -.
CC EMBL; AF281308; AAF91441.1; -.
CC EMBL; AF316894; AAK01634.1; -.
CC EMBL; AF284095; AAK26743.1; -.
CC EMBL; AY032736; AAK51162.1; -.
CC EMBL; BC050414; AAHS0414.2; -.
CC PIR; A34169; A34169.
CC PDB; 1HLL; NMR; A=118-149.
CC PDB; 1HO9; NMR; A=118-149.
CC PDB; 1HOD; NMR; A=118-149.
CC PDB; 1HOF; NMR; A=118-149.
CC Genew; HGNC:281; ADRA2A.
CC MIM; 104210; -.
CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
CC DR GO; GO:0004938; F:alpha2-adrenergic receptor activity; TAS.
CC DR GO; GO:0015459; F:potassium channel regulator activity; TAS.
CC DR GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
CC DR GO; GO:0000187; P:activation of WAPK; TAS.
CC DR GO; GO:0006928; P:cell motility; TAS.
CC DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.

DR GO; GO:0007194; P:negative regulation of adenylate cyclase ac. .; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0007265; P:RAS protein signal transduction; TAS.
DR GO; GO:0007266; P:Rho protein signal transduction; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001946; A:receptorA2Aa.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00558; ADRENRCGA2AR.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR 3D-structure; Direct protein sequencing; G-protein coupled receptor;
KW Glycoprotein; Lipoprotein; Multigene family; Palmitate;
KW Phosphorylation; Polymorphism; Transmembrane.
FT DOMAIN 1 33 Extracellular (Potential).
FT TRANSMEM 34 59 1 (Potential).
FT DOMAIN 60 70 Cytoplasmic (Potential).
FT TRANSMEM 71 96 2 (Potential).
FT DOMAIN 97 106 Extracellular (Potential).
FT TRANSMEM 107 129 3 (Potential).
FT DOMAIN 130 149 Cytoplasmic (Potential).
FT TRANSMEM 150 173 4 (Potential).
FT DOMAIN 174 192 Extracellular (Potential).
FT TRANSMEM 193 217 5 (Potential).
FT DOMAIN 218 374 Cytoplasmic (Potential).
FT TRANSMEM 375 399 6 (Potential).
FT DOMAIN 400 406 Extracellular (Potential).
FT TRANSMEM 407 430 7 (Potential).
FT DOMAIN 431 450 Cytoplasmic (Potential).
FT CARBOHYD 10 10 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 14 14 N-linked (GlcNAc. .) (Potential).
FT LIPID 106 188 By similarity.
FT LIPID 442 442 S-palmitoyl cysteine (By similarity).
FT SITE 113 113 Implicated in ligand binding.
FT SITE 200 200 Implicated in catechol agonist binding
FT SITE 204 204 and receptor activation.
FT SITE 204 204 Implicated in catechol agonist binding
FT VARIANT 251 251 and receptor activation.
FT MUTAGEN 79 N -> K (rare polymorphism; frequency in
FT MUTAGEN 113 113 Caucasians 0.004 and in African-Americans
FT MUTAGEN 130 130 0.05; 40% increase in agonist-promoted Gi
FT MUTAGEN 200 200 coupling; dbSNP:1800035).
FT MUTAGEN 200 200 /FTID-VAR_014957
FT MUTAGEN 200 200 D-N: No change in binding affinity.
FT MUTAGEN 200 200 eliminates guanine nucleotide-sensitive
FT MUTAGEN 200 200 agonist binding.
FT MUTAGEN 200 200 D-N: No binding to yohimbine. Increase
FT MUTAGEN 200 200 in adenylate cyclase activity.
FT MUTAGEN 200 200 D-N: Lower affinity for agonists.
FT MUTAGEN 200 200 Eliminates guanine nucleotide-sensitive
FT MUTAGEN 200 200 agonist binding.
FT MUTAGEN 200 200 S->A: Lower affinity for agonists. No
FT MUTAGEN 200 200
Query Match 56.1%; Score 60; DB 1; Length 450;
Best Local Similarity 63.6%; Pred. No. 89;
Matches 14; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
Qy 1 RGRPGAGARAS--GPGGAPR 20
Db 313 RGRPGKGRASQVKGDSLPR 334
RESULT 12
FUB2 RAT
ID_FUB2 RAT STANDARD; PRT; 721 AA.
AC Q9SPF5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Far upstream element binding protein 2 (FUSE binding protein 2) (KH
DE type splicing regulatory protein) (KSRP) (MAP2 RNA trans-acting
DE protein 1) (MARTAL).

GN Name=Pubp2; Synonyms=Khsrp;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 73-87; 89-108 AND 475-486, SUBCELLULAR
RP LOCATION, AND FUNCTION.
RX TISSUE=Brain;
RA MEDLINE=22246918; PubMed=12358751;
RA Rehbein M., Wege K., Buck F., Schweizer M., Richter D., Kindler S.;
RT "Molecular characterization of MARTAL, a protein interacting with the
RT dendritic targeting element of MAP2 mRNAs.";
RL J. Neurochem. 82:1039-1046 (2002).
CC -!- FUNCTION: Part of a ternary complex that binds to the downstream
CC control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in
CC transcripts that are subject to tissue-specific alternative
CC splicing. May interact with single-stranded DNA from the far-
CC upstream element (FUSE). May activate gene expression (By
CC similarity). Binds to the dendritic targeting element and may play
CC a role in mRNA trafficking.
CC -!- SUBUNIT: Part of a ternary complex containing FUBP2, PTBP1, PTBP2
CC and HNRPH1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear. A small proportion is also found in
CC the cytoplasm of neuronal cell bodies and dendrites.
CC -!- SIMILARITY: Contains 4 KH domains.
CC
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CC -----
DR EMBL; AF308818; AAC59811.1; -.
DR HSP; Q96AE4; IJ4W.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR004087; KH.
DR InterPro; IPR004088; KH_type_1.
DR Pfam; PF00013; KH; 4.
DR SMART; SM00322; KH; 4.
DR PROSITE; PSS0084; KH_TYPE_1; 4.
KW Direct protein sequencing; DNA-binding; mRNA processing;
KW mRNA splicing; mRNA transport; Nuclear protein; Repeat; RNA-binding;
KW Trans-acting factor; Transcription regulation; Transport.
FT DOMAIN 145 209 KH 1.
FT DOMAIN 234 300 KH 2.
FT DOMAIN 323 387 KH 3.
FT DOMAIN 425 492 KH 4.
FT DOMAIN 572 685 4 X 12 AA imperfect repeats.
FT REPEAT 572 583 1.
FT REPEAT 618 629 2.
FT REPEAT 644 655 3.
FT REPEAT 674 685 4.
FT DOMAIN 7 68 Gly/Pro-rich.
FT DOMAIN 69 498 Gly-rich.
FT DOMAIN 499 613 Ala/Gly/Pro-rich.
SQ SEQUENCE 721 AA; 74226 MW; 482C7A765C60EE4A CRC64;

Query Match 56.1%; Score 60; DB 1; Length 721;
Best Local Similarity 61.1%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GPRGAGARASGGGGAP 19
Db 33 GPPGAGDRGGGGGGGGP 50

RESULT 13
CE22_MOUSE
ID _CE22_MOUSE STANDARD; PRT; 926 AA.
AC QBR554;

DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Zinc finger A20 domain containing protein ? (EC 3.-.-.-) (Zinc finger
DE protein Cezanne 2).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6;
RA Evans P.C., Coadwell W.J., Kilshaw P.J.;
RT "Isolation of a novel murine gene, Cezanne 2.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Has deubiquitinating activity that is directed towards
CC lys-48 or lys-63-linked polyubiquitin chains. Hydrolyzes both
CC linear and branched forms of polyubiquitin (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the peptidase C64 family.
CC -!- SIMILARITY: Contains 1 A20-type zinc finger.
CC -!- SIMILARITY: Contains 1 OTU domain.
CC
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CC -----
DR EMBL; AJ430384; CAD23048.1; -.
DR MEROPS; C64.002; -.
DR MGD; MGI:2158505; AJ430384.
DR InterPro; IPR003323; OTU.
DR Pfam; PF02338; OTU; 1.
DR PROSITE; PSS0802; OTU; 1.
DR Zinc-finger.
KW Zinc-finger.
FT DOMAIN 170 413 TRAF-binding (By similarity).
FT DOMAIN 185 452 Catalytic (By similarity).
FT DOMAIN 201 377 OTU.
FT DOMAIN 497 512 Nuclear localization signal (Potential).
FT DOMAIN 441 926 Ubiquitin-binding (By similarity).
FT ZN_FING 890 910 A20-type (By similarity).
FT ACT_SITE 209 209 By similarity.
FT ACT_SITE 212 212 By similarity.
FT ACT_SITE 370 370 By similarity.
SQ SEQUENCE 926 AA; 100796 MW; 4D6BD05A0410BED9 CRC64;

Query Match 56.1%; Score 60; DB 1; Length 926;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGRGAGARASGGGGAPR 20
Db 739 RAARAAGGAASPGGGARR 758

RESULT 14
EPAS_RAT
ID EPAS_RAT STANDARD; PRT; 1005 AA.
AC P54757;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor EHK-1) (EPH homology kinase-1).
GN Name=EphA5; Synonyms=Ehk-1, Ekhl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
 RP STRAIN=Sprague-Dawley; TISSUE=Brain;
 RC MEDLINE=94067777; PubMed=7504232;
 RA Maisonnier P.C., Barrezaeta N.X., Yancopoulos G.D.;
 RT "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine
 RL kinase family with distinctive structures and neuronal expression.";
 [2]
 RN Oncogene 8:3277-3288(1993).
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=95206467; PubMed=7898646; DOI=10.1016/0306-4522(94)90014-0;
 RA Taylor V., Miescher G.C., Pfarr S., Honegger F., Breitschopf H.,
 RA Laessmann H., Steck A.J.;
 RT "Expression and developmental regulation of Ehk-1, a neuronal Elk-like
 RL receptor tyrosine kinase in brain.";
 CC Neurosci 63:163-178(1994).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=6;
 CC Name=1;
 CC IsoId=P54757-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P54757-2; Sequence=VSP_003001;
 CC Name=3;
 CC IsoId=P54757-3; Sequence=VSP_003002;
 CC Name=4;
 CC IsoId=P54757-4; Sequence=VSP_003002, VSP_003003;
 CC Name=5;
 CC IsoId=P54757-5; Sequence=VSP_003001, VSP_003002, VSP_003003;
 CC Name=6;
 CC IsoId=P54757-6; Sequence=VSP_003000, VSP_003002;
 CC -1- TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
 CC system. Predominantly expressed in neurons.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
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 CC -----
 CC EMBL; X78689; CAA55357.1; -.
 DR PIR; S49015; S49015.
 DR PIR; S51603; S51603.
 DR HSSP; P54763; LUPA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001090; Ephrin receptor.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN-III-like.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR008979; Gal_bind like.
 DR InterPro; IPR009030; Grow_fac recept.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF01404; Ephrin_lbd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIII.

DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
 KW Receptor; Repeat; Signal; Transferase; Transmembrane;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 26 By similarity.
 FT CHAIN 27 1005 Ephrin type-A receptor 5.
 FT DOMAIN 27 575 Extracellular (Potential).
 FT TRANSMEM 576 596 Potential.
 FT DOMAIN 597 1005 Cytoplasmic (Potential).
 FT DOMAIN 222 356 Cys-rich.
 FT DOMAIN 359 461 Fibronectin type-III 1.
 FT DOMAIN 471 561 Fibronectin type-III 2.
 FT DOMAIN 677 938 Protein kinase.
 FT DOMAIN 967 1005 SAM.
 FT NP_BIND 683 691 ATP (By similarity).
 FT BINDING 709 709 ATP (By similarity).
 FT ACT_SITE 802 802 Phosphotyrosine (by autocatalysis) (By
 FT MOD_RES 652 652 similarity).
 FT MOD_RES 658 658 Phosphotyrosine (by autocatalysis) (By
 FT MOD_RES 835 835 similarity).
 FT MOD_RES 835 835 Phosphotyrosine (by autocatalysis) (By
 FT MOD_RES 984 984 similarity).
 FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 301 301 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 425 425 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 438 438 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 10 20 GRRTQGRGG -> DADGPRAGASWCHARR (in
 FT isoform 6).
 FT FTId=VSP_003000.
 FT VCRPGFKASPHSQTKSCKPPHSYTHEASTSCVCKDYFR
 FT RESDPTMACT -> G (in isoform 2 and
 FT isoform 5).
 FT FTId=VSP_003001.
 FT RPPSAPRNAISNVNSETSFLWIPPADTGGKDVSYILCK
 FT KCNSHAGVCBECGGHYRLPQQIGLXNTSYMDADPLAHNTY
 FT TPEIEAVGVSDLSPTGTRQYVNVTTNQAA -> T (in
 FT isoform 3, isoform 4, isoform 5 and
 FT isoform 6).
 FT FTId=VSP_003002.
 FT SGSCCBGCGGRASSLCVAHPSLIW -> R (in
 FT isoform 4 and isoform 5).
 FT FTId=VSP_003003.
 FT D -> E (in Ref. 2).
 FT G -> A (in Ref. 2).
 FT G -> A (in Ref. 2).
 FT G -> A (in Ref. 2).
 FT T -> I (in Ref. 2).
 FT T -> I (in Ref. 2).
 FT CONFLICT 170 170
 FT CONFLICT 566 566
 FT CONFLICT 578 578
 FT CONFLICT 669 669
 FT CONFLICT 708 708
 FT CONFLICT 979 979
 FT SEQUENCE 1005 AA; 111007 MW; 1AED42C99693C574 CRC64;
 SQ
 Query Match 56.1%; Score 60; DB 1; Length 1005;
 Best Local Similarity 61.9%; Pred. No. 1.8e+02;
 Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
 QY 2 GPRGAGAARASGPGGG--APR 20

```
Db 5 GPRGAGRRRTQGRGGGDTPT 25
||||| | | | | |
RESULT 15
COXB_HUMAN
ID COXB_HUMAN STANDARD; PRT; 129 AA.
AC P10606; Q96J18;
DT 01-JUL-1989 (Rel. 11, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome c oxidase polypeptide Vb, mitochondrial precursor
DE (SC 1.9.3.1).
GN Name=COX5B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88284368; PubMed=2840351; DOI=10.1016/0378-1119(88)90411-8;
RA Zeviani M., Sakoda S., Sherbany A., Nakase H., Rizzuto R.,
RA Samitt C.E., Dimauro S., Schon E.A.;
RT "Sequence of cDNAs encoding subunit Vb of human and bovine cytochrome
RT c oxidase.";
RL Gene 65:1-11(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91257815; PubMed=1646156;
RA Lomax M.I., Hsieh C.L., Darras B.T., Francke U.;
RT "Structure of the human cytochrome c oxidase subunit Vb gene and
RT chromosomal mapping of the coding gene and of seven pseudogenes.";
RL Genomics 10:1-9(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 32-44.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993)
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Vb family.
```

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CC -----
CC EMBL; M59250; AAA52060.1; -;
CC EMBL; M19961; AAA52061.1; -;
CC EMBL; BC006229; AAH06229.1; -;
CC FIR; JT0324; OTHUSB.
CC SWISS-2DPAGE; P10606; HUMAN.
CC Genew; HGNC:2269; COX5B.
CC H-InvDB; HIX0002290; -;
CC MIM; 123866; -;
CC GO; GO:0004129; F.cytochrome-c oxidase activity; TAS.
CC GO; GO:0007585; P.respiratory gaseous exchange; TAS.
CC InterPro; IPR002124; COX5B.
CC Pfam; PF01215; COX5B; 1.
CC ProDom; PD007270; COX5B; 1.
CC PROSITE; PS00848; COX5B; 1.
KW Direct protein sequencing; Inner membrane; Mitochondrion;
KW Oxidoreductase; Transit peptide; Zinc.
FT TRANSIT 1 31 Mitochondrion.
FT CHAIN 32 129 Cytochrome c oxidase polypeptide Vb.
FT METAL 91 91 Zinc (Potential).
FT METAL 113 113 Zinc (Potential).
FT METAL 116 116 Zinc (Potential).
FT CONFLICT 109 109 E -> Q (in Ref. 1).
SQ SEQUENCE 129 AA; 13696 MW; 877BF4CD334AC931 CRC64;

Query Match 55.1%; Score 59; DB 1; Length 129;
Best Local Similarity 57.9%; Pred. No. 38;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGRPGAGAAARASGPGGAP 19
||| ||| | | | | |
DB 20 RGPFGAAAMRSMASGGVP 38

Search completed: September 11, 2005, 01:42:50
Job time : 28.4762 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:30:14 ; Search time 7.33333 Seconds
(without alignments)
203.588 Million cell updates/sec

Title: US-09-529-206E-4_COPY_43_62
Perfect score: 107
Sequence: 1 RGRPGAGAAASGPGGAPR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	107	100.0	180	2	US-08-791-495-9
2	107	100.0	180	4	US-09-392-714-25
3	107	100.0	180	4	US-09-165-546D-15
4	107	100.0	180	4	US-09-341-829A-9
5	107	100.0	180	4	US-09-849-602-30
6	101	94.4	180	3	US-08-917-263B-8
7	101	94.4	180	4	US-09-751-798-8
8	99	92.5	180	2	US-08-791-495-7
9	99	92.5	180	4	US-09-341-829A-7
10	99	92.5	210	2	US-08-791-495-5
11	99	92.5	210	4	US-09-341-829A-5
12	63	58.1	860	4	US-09-252-991A-25681
13	60	56.1	160	4	US-09-252-991A-27091
14	60	56.1	366	4	US-09-902-540-13196
15	60	56.1	742	4	US-09-949-016-7729
16	60	56.1	928	1	US-08-442-248-2
17	60	56.1	928	1	US-08-440-815-2
18	60	56.1	928	3	US-08-486-449-2
19	60	56.1	928	4	US-08-578-684-2
20	60	56.1	1005	2	US-08-469-537A-103
21	59	55.1	210	4	US-09-252-991A-24923
22	59	55.1	330	1	US-08-118-270-21
23	59	55.1	330	5	PCT-US93-08528-21
24	59	55.1	330	2	US-08-673-789-2
25	58	54.2	282	4	US-09-949-016-8392
26	58	54.2	456	4	US-09-252-991A-17335
27	58	54.2	700	4	US-09-252-991A-28344

28	57	53.3	416	4	US-09-270-767-43018	Sequence 43018, A
29	57	53.3	857	4	US-09-902-540-12312	Sequence 12312, A
30	56	52.3	331	4	US-09-949-016-6708	Sequence 6708, Ap
31	56	52.3	421	4	US-09-252-991A-32326	Sequence 32326, A
32	56	52.3	432	4	US-09-252-991A-23622	Sequence 23622, A
33	55	51.4	191	4	US-09-252-991A-23951	Sequence 23951, A
34	55	51.4	289	4	US-09-252-991A-25496	Sequence 25496, A
35	55	51.4	289	4	US-09-949-016-8825	Sequence 8825, Ap
36	55	51.4	343	4	US-09-252-991A-23398	Sequence 23398, A
37	54.5	50.9	501	4	US-09-252-991A-32473	Sequence 32473, A
38	54.5	50.9	608	4	US-09-464-377-2	Sequence 2, Appli
39	54.5	50.9	608	4	US-09-464-377-3	Sequence 3, Appli
40	54	50.5	140	3	US-09-220-528-5	Sequence 5, Appli
41	54	50.5	140	4	US-09-347-613C-5	Sequence 5, Appli
42	54	50.5	140	4	US-09-347-613C-10	Sequence 10, Appli
43	54	50.5	140	4	US-09-662-183A-5	Sequence 5, Appli
44	54	50.5	140	4	US-09-662-183A-10	Sequence 10, Appli
45	54	50.5	159	3	US-09-220-528-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 107; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGRPGAGAAASGPGGAPR 20
|||||
DB 43 RGRPGAGAAASGPGGAPR 62

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; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

Query Match 100.0%; Score 107; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20
Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 4
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match 100.0%; Score 107; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20
Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 5
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match 100.0%; Score 107; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20
Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 3
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; APPLICANT: Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
```


US-09-849-602-30

Query Match 100.0%; Score 107; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2,9e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGRPGAGAAASGPGGGAPR 20
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Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 6

US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 180
TYPE: amino acid
TOPOLOGY: linear

US-08-937-263B-8

Query Match 94.4%; Score 101; DB 3; Length 180;
Best Local Similarity 95.0%; Pred. No. 0.00014;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGRPGAGAAASGPGGGAPR 20
| | | | | | | | | | | | | | | | | | | | | |
Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 7

US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6525177man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 180
TYPE: amino acid
TOPOLOGY: linear

US-09-751-798-8

Query Match 94.4%; Score 101; DB 4; Length 180;
Best Local Similarity 95.0%; Pred. No. 0.00014;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGRPGAGAAASGPGGGAPR 20
| | | | | | | | | | | | | | | | | | | | | |
Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 8

US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-7

Query Match          92.5%; Score 99; DB 2; Length 180;
Best Local Similarity 95.0%; Pred. No. 0.00023;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGRGAGAAASGPGGAPR 20
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Db 43 RGRGAGAAASGPRGAPR 62

RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-341-829A-7

Query Match          92.5%; Score 99; DB 4; Length 180;
Best Local Similarity 95.0%; Pred. No. 0.00023;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGRGAGAAASGPGGAPR 20
   |||||
Db 43 RGRGAGAAASGPRGAPR 62

RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
```

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; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-5

Query Match          92.5%; Score 99; DB 2; Length 210;
Best Local Similarity 95.0%; Pred. No. 0.00027;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGRGAGAAASGPGGAPR 20
   |||||
Db 43 RGRGAGAAASGPRGAPR 62

RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-341-829A-5

Query Match          92.5%; Score 99; DB 4; Length 210;
Best Local Similarity 95.0%; Pred. No. 0.00027;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGRGAGAAASGPGGAPR 20
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Db 43 RGRGAGAAASGPRGAPR 62

RESULT 12
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US-09-252-991A-25681
; Sequence 25681, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25681
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25681
Query Match 58.9%; Score 63; DB 4; Length 860;
Best Local Similarity 63.2%; Pred. No. 11;
Matches 12; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 1 RGRGAGAAARASGFGGAP 19
| | | | | : | | | |
Db 738 RKPRGTAARQTGSGGTP 756

RESULT 13
US-09-252-991A-27091
; Sequence 27091, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27091
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27091
Query Match 56.1%; Score 60; DB 4; Length 160;
Best Local Similarity 63.6%; Pred. No. 5.3;
Matches 14; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 3 PRGAGAAARASG----PGGAP 20
| | | | | | | | | |
Db 103 PRGAGAAARASGRCRRPAGPR 124

RESULT 14
US-09-902-540-13196
; Sequence 13196, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
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US-09-902-540-13196
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13196
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13196
Query Match 56.1%; Score 60; DB 4; Length 366;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 12; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

QY 3 PRGAGAAARASGFGGAP 20
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Db 69 PRPAGTAPAAAGPGATAPR 86

RESULT 15
US-09-949-016-7729
; Sequence 7729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTIER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7729
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7729
Query Match 56.1%; Score 60; DB 4; Length 742;
Best Local Similarity 61.1%; Pred. No. 22;
Matches 11; Conservative 0; Mismatches 7; Indels 7; Gaps 0;

QY 2 GPRGAGAAARASGFGGAP 19
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Db 64 GPPGAGDRGGGFGGGGP 81

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:43:05 ; Search time 27.0476 Seconds
(without alignments)
291.657 Million cell updates/sec

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Perfect score: 107
Sequence: 1 RGRPGAGAAASGPGGAPR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	107	100.0	179	17	US-10-482-029-202
2	107	100.0	180	10	US-09-849-602-30
3	107	100.0	180	14	US-10-207-655-71
4	107	100.0	180	15	US-10-026-066-3
5	107	100.0	180	15	US-10-117-937-74
6	107	100.0	180	15	US-10-295-027-386
7	107	100.0	180	15	US-10-296-734-832
8	107	100.0	180	15	US-10-188-832-139
9	107	100.0	180	16	US-10-777-053-11
10	107	100.0	180	16	US-10-751-088-15
11	107	100.0	180	16	US-10-657-022-74
12	107	100.0	179	17	US-10-482-029-202
13	107	100.0	180	10	US-09-849-602-30
14	107	100.0	180	14	US-10-207-655-71
15	107	100.0	180	15	US-10-026-066-3
16	107	100.0	180	15	US-10-117-937-74
17	107	100.0	180	15	US-10-295-027-386
18	107	100.0	180	15	US-10-296-734-832
19	107	100.0	180	15	US-10-188-832-139
20	107	100.0	180	16	US-10-777-053-11
21	107	100.0	180	16	US-10-751-088-15
22	107	100.0	180	16	US-10-657-022-74

12	107	100.0	180	16	US-10-837-217-11	Sequence 11, Appl
13	107	100.0	180	16	US-10-877-373-9	Sequence 9, Appl
14	107	100.0	180	16	US-10-723-860-1270	Sequence 1270, Ap
15	107	100.0	180	17	US-10-871-708-7	Sequence 7, Appl
16	107	100.0	180	18	US-10-895-523-3	Sequence 3, Appl
17	107	100.0	180	18	US-10-182-508A-3	Sequence 3, Appl
18	107	100.0	180	18	US-10-756-149-5024	Sequence 5024, Ap
19	107	100.0	180	20	US-11-067-064-74	Sequence 74, Appl
20	107	100.0	337	9	US-09-821-883-27	Sequence 27, Appl
21	102	95.3	30	15	US-10-296-734-1404	Sequence 1404, Ap
22	102	95.3	3541	15	US-10-296-734-1454	Sequence 1454, Ap
23	101	94.4	180	9	US-09-751-798-8	Sequence 8, Appl
24	101	94.4	180	13	US-10-023-182-8	Sequence 14, Appl
25	101	94.4	180	14	US-10-364-614-14	Sequence 368, App
26	99	92.5	135	15	US-10-295-027-388	Sequence 141, App
27	99	92.5	135	15	US-10-188-832-141	Sequence 69, Appl
28	99	92.5	180	14	US-10-146-473-69	Sequence 75, Appl
29	99	92.5	180	15	US-10-117-937-75	Sequence 834, App
30	99	92.5	180	15	US-10-296-734-834	Sequence 4, Appl
31	99	92.5	180	16	US-10-468-406-4	Sequence 7, Appl
32	99	92.5	180	16	US-10-877-373-7	Sequence 7, Appl
33	99	92.5	180	20	US-11-067-064-75	Sequence 75, Appl
34	99	92.5	210	14	US-10-157-031-88	Sequence 88, Appl
35	99	92.5	210	15	US-10-117-937-76	Sequence 76, Appl
36	99	92.5	210	16	US-10-657-022-76	Sequence 5, Appl
37	99	92.5	210	16	US-10-877-373-5	Sequence 76, Appl
38	99	92.5	210	20	US-11-067-064-76	Sequence 76, Appl
39	99	92.5	210	20	US-10-313-986-496	Sequence 496, App
40	95	88.8	20	16	US-10-775-972-496	Sequence 496, App
41	95	88.8	20	18	US-10-922-124-496	Sequence 1436, Ap
42	95	88.8	30	15	US-10-296-734-1436	Sequence 1402, Ap
43	94	87.9	30	15	US-10-296-734-1436	Sequence 1434, Ap
44	85	79.4	30	15	US-10-296-734-1402	
45	77	72.0	30	15	US-10-296-734-1434	

ALIGNMENTS

RESULT 1

US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

Query Match 100.0%; Score 107; DB 17; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGAPR 20

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Db 43 RGRPGAGAAASGPGGAPR 62

RESULT 2

US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.

```
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseeng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match      100.0%; Score 107; DB 10; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGRGAGAAARASGPGGGAPR 20
Db      43 RGRGAGAAARASGPGGGAPR 62

RESULT 3
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-71

Query Match      100.0%; Score 107; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGRGAGAAARASGPGGGAPR 20
Db      43 RGRGAGAAARASGPGGGAPR 62

RESULT 4
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTILMM.21CPIC
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27

; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseeng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match      100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGRGAGAAARASGPGGGAPR 20
Db      43 RGRGAGAAARASGPGGGAPR 62

RESULT 5
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTILMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match      100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGRGAGAAARASGPGGGAPR 20
Db      43 RGRGAGAAARASGPGGGAPR 62

RESULT 6
US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
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; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match 100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAASGPGGAPR 20
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DB 43 RGRGAGAAASGPGGAPR 62

RESULT 7

US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 832
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA consensus polypeptide
US-10-296-734-832

Query Match 100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAASGPGGAPR 20
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DB 43 RGRGAGAAASGPGGAPR 62

RESULT 8

US-10-188-832-139

; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Azi, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAASGPGGAPR 20
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DB 43 RGRGAGAAASGPGGAPR 62

RESULT 9

US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-777-053-11

Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAASGPGGAPR 20
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DB 43 RGRGAGAAASGPGGAPR 62

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RESULT 10
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CH
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10751.088
; FILING DATE: 02-Jan-2004
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15
Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAARASGPGGAPR 20
Db 43 RGPRGAGAAARASGPGGAPR 62

RESULT 11
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022

US-10-837-217-11
; Sequence 11, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-837-217-11
Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAARASGPGGAPR 20
Db 43 RGPRGAGAAARASGPGGAPR 62

RESULT 13
US-10-877-373-9
; Sequence 9, Application US/10877373
; Publication No. US20040234541A1
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/10/877,373
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/341,829
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
<151> 1997-01-27
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; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022-74
Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAARASGPGGAPR 20
Db 43 RGPRGAGAAARASGPGGAPR 62

RESULT 12
US-10-837-217-11
; Sequence 11, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-837-217-11
Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAARASGPGGAPR 20
Db 43 RGPRGAGAAARASGPGGAPR 62

RESULT 13
US-10-877-373-9
; Sequence 9, Application US/10877373
; Publication No. US20040234541A1
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/10/877,373
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/341,829
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
<151> 1997-01-27
<151> 1998-01-27
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; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-877-373-9

Query Match 100.0%; Score 107; DB 16; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGPGGAPR 20
Db 43 RGRGAGAAARASGPGGAPR 62

RESULT 14

US-10-723-860-1270

; Sequence 1270, Application US/10723860

; Publication No. US20040253606A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsburg, Wendy M.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01

; CURRENT APPLICATION NUMBER: US/10/723,860

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 60/429,739

; PRIOR FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 8393

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1270

; LENGTH: 180

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-723-860-1270

Query Match 100.0%; Score 107; DB 16; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGPGGAPR 20
Db 43 RGRGAGAAARASGPGGAPR 62

RESULT 15

US-10-871-708-7

; Sequence 7, Application US/10871708

; Publication No. US20050118186A1

; GENERAL INFORMATION:

; APPLICANT: Chiang, Chih-Sheng

; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

; FILE REFERENCE: MANNK.035A

; CURRENT APPLICATION NUMBER: US/10/871,708

; CURRENT FILING DATE: 2004-06-17

; PRIOR APPLICATION NUMBER: 60/479,554

; PRIOR FILING DATE: 2003-06-17

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 180

; TYPE: PRT

; ORGANISM: Autoimmunogenic Cancer

US-10-871-708-7

Query Match 100.0%; Score 107; DB 17; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGPGGAPR 20
Db 43 RGRGAGAAARASGPGGAPR 62

Search completed: September 11, 2005, 02:07:10
Job time : 27.0476 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:19:58 ; Search time 14.3333 Seconds
(without alignments)
269.833 Million cell updates/sec

Title: US-09-529-206E-4_COPY_127_136

Perfect score: 47

Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	10	2	Aay05980 Human can
2	47	100.0	10	2	Aay05988 Human can
3	47	100.0	10	4	Aae07788 Human NY
4	47	100.0	14	4	Aae07728 Human NY
5	47	100.0	15	4	Aae07726 Human NY
6	47	100.0	15	4	Aae07727 Human NY
7	47	100.0	15	4	Aae07786 Human NY
8	47	100.0	15	4	Aae07787 Human NY
9	47	100.0	18	3	Aay52440 Human tum
10	47	100.0	18	4	Aab69940 Human NY-
11	47	100.0	18	4	Aab69944 Human NY-
12	47	100.0	18	4	AAU01544 HLA-DR53
13	47	100.0	18	4	AAU01540 HLA-DR53
14	47	100.0	18	4	Aae07769 Human NY
15	47	100.0	20	4	Aae07742 Human ESO
16	47	100.0	20	8	ADI19891 Human HLA
17	47	100.0	20	8	ADI19048 Human HLA
18	47	100.0	20	8	ADJ58397 Peptide p
19	47	100.0	25	4	Aae07718 Human NY
20	47	100.0	25	7	ADD71521 HLA-DP4 b
21	47	100.0	27	4	Aae07717 Human NY
22	47	100.0	30	5	AAU85110 Human NYN
23	47	100.0	36	5	ABG79131 Human NY-
24	47	100.0	54	8	ADG89697 Class II
25	47	100.0	123	8	ADQ10452 Epitope 1

26	47	100.0	179	8	ADK68648	Adk68648 Epitope 1
27	47	100.0	179	8	ADK68657	Adk68657 Epitope 1
28	47	100.0	179	8	ADQ10455	Adq10455 Epitope 1
29	47	100.0	180	2	AAW62584	Aaw62584 Cancer ae
30	47	100.0	180	2	AAW69655	Aaw69655 Human NY-
31	47	100.0	180	2	AAW05955	Aaw05955 Human can
32	47	100.0	180	3	AAW52430	Aaw52430 Human tum
33	47	100.0	180	3	AAW70862	Aaw70862 Human oes
34	47	100.0	180	3	AAW03154	Aaw03154 Human oes
35	47	100.0	180	4	AAW69946	Aaw69946 Human NY-
36	47	100.0	180	4	AAW67164	Aaw67164 Amino aci
37	47	100.0	180	4	AAU01535	AAu01535 Human NY-
38	47	100.0	180	4	AAE07714	AAe07714 Human NY
39	47	100.0	180	5	AAU84818	AAu84818 Human NYN
40	47	100.0	180	5	AAU11543	AAu11543 Human tum
41	47	100.0	180	6	ABR58572	ABr58572 Human can
42	47	100.0	180	6	ABR48210	ABr48210 Human bla
43	47	100.0	180	6	ABU56508	ABu56508 Lung canc
44	47	100.0	180	6	ABU56694	ABu56694 Lung canc
45	47	100.0	180	6	ABP74198	ABp74198 Human NY-

ALIGNMENTS

RESULT 1
AAY05980
ID AAY05980 standard; peptide; 10 AA.
XX AC AAY05980;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide ESO10-127.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX OS Homo sapiens.
XX
XX
PN WO9918206-A2.
XX
XX
PD 15-APR-1999.
XX
XX
PF 21-SEP-1998; 98WO-US019609.
XX
XX
PR 08-OCT-1997; 97US-0061428P.
XX
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
XX
DR WPI; 1999-277270/23.
XX
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
XX
PS Claim 17; Page 64; 88pp; English.
XX
XX
CC This sequence represents cancer peptide ESO10-127 that corresponds to
CC amino acid residues 127-136 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC AAY05986), a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides derived from
CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC variants (see AAY05967-87), are useful as cancer vaccines that protect
CC against cancer. The invention provides: vectors and host cells (also
CC useful as vaccines); a method of diagnosis of cancer or precancer; a
CC transgenic animal; antisense oligonucleotides that inhibit expression of
CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3

CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 47; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 DB 1 TVSGNLTIR 10

RESULT 2
 AAY05988
 ID AAY05988 standard; peptide; 10 AA.

AC AAY05988;

XX
 DT 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; human leukocyte antigen; HLA.

XX Homo sapiens.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

XX Example 10; Page 42; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a screen
 CC for epitopes from the coding region of human NY ESO-1/CAG-3 ORF1 (see
 CC AX58599). 30 Epitopes (see AAY05988-Y06017) were identified. The present
 CC peptide (ranked 1) corresponds to amino acid residues 127-136 of CAG-1
 CC ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of
 CC eliciting an antigen specific immune response by T cells. Cancer peptides
 CC (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their
 CC variants, are useful as cancer vaccines. A claimed method of preventing
 CC or inhibiting cancer involves administering a cancer peptide, with or
 CC without an HLA molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
 CC prostate, ovarian, pancreatic and thyroid cancers

XX Sequence 10 AA;

Query Match 100.0%; Score 47; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 DB 1 TVSGNLTIR 10

RESULT 3
 AAE07788
 ID AAE07788 standard; peptide; 14 AA.

XX AAE07788;

XX 06-NOV-2001 (first entry)

XX Human NY ESO-1 peptide #22 to characterise epitope recognised by TE4-1.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.

XX Example 6; Fig 6A; 134pp; English.

XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leukocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC peptide used in the characterisation of the NY ESO-1 epitope recognised
 CC by TE4-1

XX Sequence 14 AA;

XX Query Match 100.0%; Score 47; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
DB 4 TVSGNLTIR 13

RESULT 4
AAE07728
ID AAE07728 standard; peptide; 14 AA.
XX
AC AAE07728;

XX 06-NOV-2001 (first entry)

XX Human NY ESO-1 MHC class II restricted T cell epitope #14.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.

XX Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is MHC class II
CC restricted T cell epitope of human NY ESO-1 protein

XX Sequence 14 AA;

Query Match 100.0%; Score 47; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
DB 4 TVSGNLTIR 13

DB 4 TVSGNLTIR 13

RESULT 5

AAE07726
ID AAE07726 standard; peptide; 15 AA.
XX
XX AAE07726;

XX 06-NOV-2001 (first entry)

XX Human NY ESO-1 MHC class II restricted T cell epitope #12.
XX
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.

XX Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is MHC class II
CC restricted T cell epitope of human NY ESO-1 protein

XX Sequence 15 AA;

Query Match 100.0%; Score 47; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
DB 6 TVSGNLTIR 15

RESULT 6
AAE07727

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ID  AAE07727 standard; peptide; 15 AA.
XX
AC  AAE07727;
XX
DT  06-NOV-2001 (first entry)
XX
DE  Human NY ESO-1 MHC class II restricted T cell epitope #13.
XX
KW  Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW  class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW  NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW  tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW  immunotherapy.
XX
OS  Homo sapiens.
XX
PN  WO200155393-A2.
XX
PD  02-AUG-2001.
XX
PF  26-JAN-2001; 2001WO-US002765.
XX
PR  28-JAN-2000; 2000US-0179004P.
XX
PR  29-SEP-2000; 2000US-0237107P.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Wang R, Rosenberg SA, Zeng G;
XX
PI  WPI; 2001-496851/54.
XX
PT  New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT  useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT  protection from metastasis.
XX
PS  Claim 4; Page 16; 134pp; English.
XX
CC  The invention relates to the identification and isolation of major
CC  histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC  epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC  from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC  antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC  restricted. The products of the gene are promising candidates for
CC  immunotherapeutic strategies for the prevention, treatment and diagnosis
CC  of patients with cancer. The cancer epitopes are useful as immunogen and
CC  vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC  lymphocytes resulting in protection of the recipient from development of
CC  cancer and protection from metastasis, or by inhibiting the growth of
CC  cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC  useful as diagnostic agent to detect the presence of cancer, to enhance
CC  the generation of antibody and/or CD8+ T cell responses against any given
CC  target antigen and/or hapten and to induce tumour-specific humoral-
CC  mediated immunity against cancer. The present sequence is MHC class II
CC  restricted T cell epitope of human NY ESO-1 protein
XX
SQ  Sequence 15 AA;

Query Match      100.0%; Score 47; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TVSGNLTIR 10
    |||||
Db  5 TVSGNLTIR 14

RESULT 7
AAE07786
ID  AAE07786 standard; peptide; 15 AA.
XX
AC  AAE07786;
XX
DT  06-NOV-2001 (first entry)
XX

```

```

XX  Human NY ESO-1 peptide #20 to characterise epitope recognised by TE4-1.
DE
XX  Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW  class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW  NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW  tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW  immunotherapy.
XX
OS  Homo sapiens.
XX
PN  WO200155393-A2.
XX
PD  02-AUG-2001.
XX
PF  26-JAN-2001; 2001WO-US002765.
XX
PR  28-JAN-2000; 2000US-0179004P.
XX
PR  29-SEP-2000; 2000US-0237107P.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Wang R, Rosenberg SA, Zeng G;
XX
PI  WPI; 2001-496851/54.
XX
PT  New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT  useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT  protection from metastasis.
XX
PS  Example 6; Fig 6A; 134pp; English.
XX
CC  The invention relates to the identification and isolation of major
CC  histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC  epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC  from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC  antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC  restricted. The products of the gene are promising candidates for
CC  immunotherapeutic strategies for the prevention, treatment and diagnosis
CC  of patients with cancer. The cancer epitopes are useful as immunogen and
CC  vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC  lymphocytes resulting in protection of the recipient from development of
CC  cancer and protection from metastasis, or by inhibiting the growth of
CC  cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC  useful as diagnostic agent to detect the presence of cancer, to enhance
CC  the generation of antibody and/or CD8+ T cell responses against any given
CC  target antigen and/or hapten and to induce tumour-specific humoral-
CC  mediated immunity against cancer. The present sequence is human NY ESO-1
CC  peptide used in the characterisation of the NY ESO-1 epitope recognised
CC  by TE4-1
XX
SQ  Sequence 15 AA;

Query Match      100.0%; Score 47; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TVSGNLTIR 10
    |||||
Db  6 TVSGNLTIR 15

RESULT 8
AAE07787
ID  AAE07787 standard; peptide; 15 AA.
XX
AC  AAE07787;
XX
DT  06-NOV-2001 (first entry)
XX
DE  Human NY ESO-1 peptide #21 to characterise epitope recognised by TE4-1.
XX
DE  Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW

```

KW Class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155393-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-US002765.
 XX
 PR 28-JAN-2000; 2000US-0179004P.
 PR 29-SEP-2000; 2000US-0237107P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wang R, Rosenberg SA, Zeng G;
 XX WPI; 2001-496851/54.
 DR
 XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.
 XX
 PS Example 6; Fig 6A; 134pp; English.
 XX
 CC The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leukocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC peptide used in the characterisation of the NY ESO-1 epitope recognised
 CC by TE4-1
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 47; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVSGNLTIR 10
 DB 5 TVSGNLTIR 14
 |||||
 RESULT 9
 AAY52440
 ID AAY52440 standard; protein; 18 AA.
 XX
 AC AAY52440;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Human tumour antigen NY-ESO-1 peptide #13.
 XX
 KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
 KW T-cell; helper; stimulation; proliferation; treatment; diagnosis;
 KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
 KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
 XX

OS Synthetic.
 OS Homo sapiens.
 PN WO9953938-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US006875.
 XX
 PR 17-APR-1998; 98US-00062422.
 PR 02-OCT-1998; 98US-00165546.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
 PI Gure A, Ritter G;
 DR WPI; 2000-038483/03.
 XX
 PT Novel peptides which bind to MHC class I and MHC class II molecules,
 PT useful for therapeutic and diagnostic purposes.
 XX
 PS Claim 4; Page 22; 49pp; English.
 XX
 CC Peptides #8-#13 (AAY52435-Y52440) are peptides derived from the human
 CC tumour antigen, NY-ESO-1 (AAY52430) which can bind to MHC(major
 CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
 CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
 CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
 CC localisation studies revealed it to be expressed at high levels in normal
 CC ovary and testis but not in normal colon, kidney, liver, brain,
 CC oesophagus and skin. It was expressed in certain tumours and tumour cell
 CC lines with some degree of frequency - these included melanoma specimens
 CC and cell lines, and breast and bladder cancer specimens, with expression
 CC in other tumour types being sporadic. These NY-ESO-1-derived peptides may
 CC be used in methods and compositions used for the treatment, diagnosis and
 CC prevention of cancers (such as melanoma, breast cancer, prostate cancer,
 CC lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or
 CC lymphoma) and to stimulate the proliferation of T cells
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 47; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVSGNLTIR 10
 DB 1 TVSGNLTIR 10
 |||||
 RESULT 10
 AAB69940
 ID AAB69940 standard; peptide; 18 AA.
 XX
 AC AAB69940;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Human NY-ESO-1 HLA-DR53 binding motif #2.
 XX
 KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX
 OS Homo sapiens.
 XX
 PN WO200107917-A1.
 XX
 PD 01-FEB-2001.
 XX
 PR 14-JUL-2000; 2000WO-US019220.
 XX

PR 23-JUL-1999; 99US-00359503.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX (CORR) CORNELL RES FOUND INC.
 XX
 PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 XX WPI; 2001-182822/18.
 DR
 XX
 XX Method useful for determining the status (e.g. progression, regression or
 PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.
 XX
 XX Example 16; Page 27; 50pp; English.
 PS
 XX The present sequence is given in a specification relating to a method for
 XX determining the status of a cancerous condition in a patient with a
 CC tumour that expresses NY-ESO-1. The method comprises assaying a sample
 CC taken from the patient for antibodies that specifically bind to the NY-
 CC ESO-1 and comparing the value obtained to a prior value obtained from
 CC assay of a prior sample taken from the patient. Any difference between
 CC the values is indicative of a change in status of the cancerous
 CC condition. The method is useful for determining whether a cancerous
 CC condition is progressing, regressing or remaining stable, in particular
 CC in patients receiving treatment for a melanoma, adenocarcinoma, non-small
 CC cell lung carcinoma or bladder carcinoma
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 47; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVSGNLTIR 10
 DB 7 TVSGNLTIR 16
 RESULT 11
 AAB69944
 ID AAB69944 standard; peptide; 18 AA.
 AC AAB69944;
 XX
 XX 27-APR-2001 (first entry)
 DT
 XX
 XX Human NY-ESO-1 HLA-DR53 binding motif #6.
 DE
 XX
 XX Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX
 XX Homo sapiens.
 OS
 XX WO200107917-A1.
 PN
 XX 01-FEB-2001.
 PD
 XX
 XX 14-JUL-2000; 2000WO-US019220.
 PF
 XX 23-JUL-1999; 99US-00359503.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX (CORR) CORNELL RES FOUND INC.
 XX
 XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 PI WPI; 2001-182822/18.
 XX
 XX Method useful for determining the status (e.g. progression, regression or

PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.
 XX
 XX Example 16; Page 28; 50pp; English.
 PS
 XX The present sequence is given in a specification relating to a method for
 XX determining the status of a cancerous condition in a patient with a
 CC tumour that expresses NY-ESO-1. The method comprises assaying a sample
 CC taken from the patient for antibodies that specifically bind to the NY-
 CC ESO-1 and comparing the value obtained to a prior value obtained from
 CC assay of a prior sample taken from the patient. Any difference between
 CC the values is indicative of a change in status of the cancerous
 CC condition. The method is useful for determining whether a cancerous
 CC condition is progressing, regressing or remaining stable, in particular
 CC in patients receiving treatment for a melanoma, adenocarcinoma, non-small
 CC cell lung carcinoma or bladder carcinoma
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 47; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVSGNLTIR 10
 DB 1 TVSGNLTIR 10
 RESULT 12
 AAU01544
 ID AAU01544 standard; peptide; 18 AA.
 XX
 XX AAU01544;
 AC
 XX 18-JUL-2001 (first entry)
 DT
 XX
 XX HLA-DR53 recognising NY-ESO-1 peptide #6.
 DE
 XX
 XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.
 XX
 XX Homo sapiens.
 OS
 XX WO200123560-A2.
 PN
 XX 05-APR-2001.
 PD
 XX 26-SEP-2000; 2000WO-US026411.
 PF
 XX 29-SEP-1999; 99US-00408036.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Tureci O, Sahin U, Pfreundschuh M;
 PI WPI; 2001-266156/27.
 XX
 XX Polypeptides binding to major histocompatibility complex class II human
 PT leukocyte antigen-determining region molecule having amino acid sequence
 PT found in tumor rejection antigen precursor used for stimulating
 PT proliferation of helper T cells.
 XX
 XX Example 13; Page 19; 62pp; English.
 PS
 XX The sequence represents a human NY-ESO-1 tumour rejection antigen
 CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
 CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
 CC complex (MHC) Class II molecules such as human leukocyte antigen-
 CC determining region (HLA-DR) molecules and stimulate proliferation of

CC helper T cells. The peptides can be administered to an HLA-DR positive
 CC subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-
 CC NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in
 CC free form is useful for this stimulation. The nucleic acid is useful for
 CC screening for a cancerous condition, which involves contacting a subject
 CC sample to a cell line transfected with the immunoreactive cell (helper T
 CC cell), where interaction is indicative of cancer. In addition, a sample
 CC from a patient (for example, a body fluid or tissue) can be monitored for
 CC the amount of the complex present in the bloodstream. This is useful for
 CC determining regression, progression or onset of a cancerous condition.
 CC The method involves contacting the sample with a radioactive labelled or
 CC enzyme labelled monoclonal antibody which specifically binds with the
 CC complex

XX Sequence 18 AA;
 SQ Query Match 100.0%; Score 47; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 DB 1 TVSGNLTIR 10
 |||||

RESULT 13
 AAU01540
 ID AAU01540 standard; peptide; 18 AA.

AC AAU01540;
 XX 18-JUL-2001 (first entry)

DE HLA-DR53 recognising NY-ESO-1 peptide #2.

XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.

XX Homo sapiens.

XX WO200123560-A2.

XX 05-APR-2001.

XX 26-SEP-2000; 2000WO-US026411.

XX 29-SEP-1999; 99US-00408036.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Tureci O, Sahin U, Pfreundschuh M;

XX WPI; 2001-266156/27.

XX Polypeptides binding to major histocompatibility complex class II human
 PT leukocyte antigen-determining region molecule having amino acid sequence
 PT found in tumor rejection antigen precursor used for stimulating
 PT proliferation of helper T cells.

XX Example 13; Page 19; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen
 CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
 CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
 CC complex (MHC) Class II molecules such as human leukocyte antigen-
 CC determining region (HLA-DR) molecules and stimulate proliferation of
 CC helper T cells. The peptides can be administered to an HLA-DR positive
 CC subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-
 CC NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in
 CC free form is useful for this stimulation. The nucleic acid is useful for

CC screening for a cancerous condition, which involves contacting a subject
 CC sample to a cell line transfected with the immunoreactive cell (helper T
 CC cell), where interaction is indicative of cancer. In addition, a sample
 CC from a patient (for example, a body fluid or tissue) can be monitored for
 CC the amount of the complex present in the bloodstream. This is useful for
 CC determining regression, progression or onset of a cancerous condition.
 CC The method involves contacting the sample with a radioactive labelled or
 CC enzyme labelled monoclonal antibody which specifically binds with the
 CC complex

XX Sequence 18 AA;

SQ Query Match 100.0%; Score 47; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 DB 7 TVSGNLTIR 16
 |||||

RESULT 14
 AAE07769
 ID AAE07769 standard; peptide; 18 AA.

XX AAE07769;

XX 06-NOV-2001 (first entry)

XX Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.

XX Claim 84; Page 84; 134pp; English.

XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leukocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance

CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human NY ESO-1
CC HLA DR restricted T cell cancer peptide

XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 15

AAE07742
ID AAE07742 standard; peptide; 20 AA.

AC AAE07742;

DT 06-NOV-2001 (first entry)

DE Human ESO p126-145 peptide, to identify MHC class II-restricted epitopes.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.

XX Example 3; Fig 3; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human ESO p126-
CC 145 peptide used in the identification of putative MHC class II -
CC restricted epitopes from HLA-DR4-transgenic mice

XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 47; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 2 TVSGNLTIR 11

Search completed: September 11, 2005, 01:38:05
Job time : 15.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:28:54 ; Search time 2.80952 Seconds
(without alignments)
342.466 Million cell updates/sec.

Title: US-09-529-206E-4_COPY_127_136

Perfect score: 47

Sequence: 1 TVSGNLTITR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	76.6	245	2 T13099	major tail protein
2	36	76.6	323	2 AD2753	lipic Acid Synthe
3	36	76.6	323	2 B97534	lipic acid synthe
4	35	74.5	335	2 A89837	hypothetical prote
5	34	72.3	177	1 R5BS0F	ribosomal protein
6	34	72.3	244	2 T41234	translation initia
7	34	72.3	311	2 AB3218	2-hydroxyacid dehy
8	34	72.3	314	2 G86835	hypothetical prote
9	34	72.3	1266	2 A85989	hypothetical prote
10	34	72.3	1266	2 F91143	hypothetical prote
11	33	70.2	144	1 TPBP1	tail fiber protein
12	33	70.2	144	2 S18683	gene R protein - E
13	33	70.2	411	2 G95241	MATE efflux family
14	33	70.2	426	2 B98106	hypothetical prote
15	33	70.2	428	2 F85253	hypothetical prote
16	33	70.2	436	2 B81033	N-acetylglutamate
17	33	70.2	436	2 A81977	probable amino-aci
18	33	70.2	449	2 S02011	serotonin receptor
19	33	70.2	471	2 A43956	serotonin receptor
20	33	70.2	471	2 S11280	serotonin receptor
21	33	70.2	471	2 S40589	5-hydroxytryptamin
22	33	70.2	471	2 A34863	serotonin receptor
23	33	70.2	876	2 E06574	hypothetical prote
24	33	70.2	918	2 T02759	hypothetical prote
25	33	70.2	1996	2 F71405	probable TWV resis
26	32	68.1	102	2 C86898	hypothetical prote
27	32	68.1	121	2 B81972	probable integral
28	32	68.1	135	2 B81029	conserved hypothet
29	32	68.1	187	2 I37105	5-Htr2c receptor -

30 32 68.1 234 2 H75390 hypothetical prote
31 32 68.1 245 2 S57550 hypothetical prote
32 32 68.1 289 2 C87158 probable oxidoredu
33 32 68.1 316 2 S25234 lysozyme (EC 3.2.1
34 32 68.1 344 2 A69325 hypothetical prote
35 32 68.1 347 2 G95146 conserved domain p
36 32 68.1 347 2 E98014 conserved hypothet
37 32 68.1 376 2 C97059 uncharacterized pr
38 32 68.1 418 2 E70401 S-adenosylhomocyst
39 32 68.1 451 2 S65162 hypothetical prote
40 32 68.1 455 1 HMXRS3 sigma 1 protein pr
41 32 68.1 458 2 JS0616 serotonin receptor
42 32 68.1 459 2 A43951 serotonin receptor
43 32 68.1 460 2 A32605 serotonin receptor
44 32 68.1 479 2 S23562 serotonin receptor
45 32 68.1 491 2 T30590 alkylhalidase homo

ALIGNMENTS

RESULT 1

T13099

major tail protein V - phage N15

N;Alternate names: protein gpl3

C;Species: phage N15

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C;Accession: T13099

R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.

submitted to the EMBL Data Library, May 1998

A;Reference number: Z17603

A;Accession: T13099

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-245 <H>

A;Cross-references: UNIPROT:O64327; EMBL:AF064539; NID:G3192683; PID:G3192697; PIDN:AACT

C;Genetics:

A;Note: Gene 13

C;Superfamily: phage lambda major tail protein V

Query Match 76.6%; Score 36; DB 2; Length 245;

Best Local Similarity 77.8%; Pred. No. 14;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIT 9

Db 209 TVSGNLTITV 217

RESULT 2

AD2753

lipic Acid Synthetase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: AD2753

R;Wood, D.W.; Scubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Y.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AD2753

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-323 <KUR>

A;Cross-references: UNIPROT:Q8UFG1; GB:AE008688; PIDN:AAI42442.1; PID:gl7739856; GSPDB:

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: lipA

A;Map position: circular chromosome

C;Superfamily: lipic acid synthase

Query Match 76.6%; Score 36; DB 2; Length 323;
 Best Local Similarity 70.0%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 Db 189 TVFGNLTVR 198

RESULT 3

B97534
 lipolic acid synthetase (lip-syn) (lipoate synthase) [imported] - Agrobacterium tumefaciens
 C;Species: Agrobacterium tumefaciens
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: B97534
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: B97534
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-323 <KUR>
 A;Cross-references: UNIPROT:Q8UFG1; GB:AE007869; PIDN:AAK87227.1; PID:gl5156511; GSPDB:C
 C;Genetics:
 A;Gene: AGR_C_2646
 A;Map position: circular chromosome
 C;Superfamily: lipolic acid synthase

Query Match 76.6%; Score 36; DB 2; Length 323;
 Best Local Similarity 70.0%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 Db 189 TVFGNLTVR 198

RESULT 4

A89837
 hypothetical protein SA0619 [imported] - Staphylococcus aureus (strain N315)
 C;Species: Staphylococcus aureus
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C;Accession: A89837
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: A89837
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-335 <KUR>
 A;Cross-references: UNIPROT:Q99VW7; GB:BA000018; PID:gl3700555; PIDN:BA041852.1; GSPDB:C
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: SA0619
 C;Superfamily: probable sodium-dependent phosphate transporter MTH1885

Query Match 74.5%; Score 35; DB 2; Length 335;
 Best Local Similarity 70.0%; Pred. No. 30;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 Db 245 TVGNIMKIR 254

RESULT 5

R5BS0F
 2-hydroxyacid dehydrogenase Atu5474 [imported] - Agrobacterium tumefaciens (strain C58,

ribosomal protein L6 - Bacillus stearothermophilus

N;Alternate names: ribosomal protein BL10
 C;Species: Bacillus stearothermophilus
 C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
 C;Accession: A02766; B39085; S59061
 R;Kimura, M.; Rawlings, N.; Appelt, K.; FEBS Lett. 136, 58-64, 1981
 A;Title: The amino acid sequence of protein BL10 from the 50S subunit of the Bacillus stearothermophilus 70S ribosome
 A;Reference number: A02766
 A;Accession: A02766
 A;Molecule type: protein
 A;Residues: 1-177 <KIM>
 A;Cross-references: UNIPROT:P02391
 R;Ramakrishnan, V.; Garckman, S.E.; J. Biol. Chem. 266, 880-885, 1991
 A;Title: Cloning, sequencing, and overexpression of genes for ribosomal proteins from Bacillus stearothermophilus
 A;Reference number: A39085; MUID:91093287; PMID:1985969
 A;Accession: B39085

A;Molecule type: DNA

A;Residues: 8-170 <RAM>
 A;Cross-references: GB:M57622
 R;Urbau, H.; Kruff, V.; Bischof, O.; Mueller, E.C.; Wittmann-Liebold, B.; EMBO J. 14, 4578-4588, 1995

A;Title: Protein-rRNA binding features and their structural and functional implications
 A;Reference number: S59051; MUID:96003638; PMID:7556101
 A;Accession: S59061

A;Molecule type: protein

A;Residues: 149-163 <URL>
 C;Superfamily: ribosomal protein L6/L9
 C;Keywords: protein biosynthesis; ribosome

Query Match 72.3%; Score 34; DB 1; Length 177;
 Best Local Similarity 55.6%; Pred. No. 25;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
 |||||
 Db 43 TVEGNVITV 51

RESULT 6

T41234
 translation initiation factor eIF-6 [imported] - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T41234
 R;Lyne, M.; Harris, D.E.; Murphey, L.D.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, January 1999
 A;Reference number: Z21979
 A;Accession: T41234
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-244 <LYN>
 A;Cross-references: UNIPROT:O94476; EMBL:AL035075; PIDN:CAA22640.1; GSPDB:GN00068; SPDB:G000068
 A;Experimental source: strain 972h-; cosmid c1919
 C;Genetics:
 A;Gene: SPDB:SPCC1919.09
 A;Map position: 3
 A;Introns: 12/2; 36/2
 C;Superfamily: conserved hypothetical protein YPR016C

Query Match 72.3%; Score 34; DB 2; Length 244;
 Best Local Similarity 75.0%; Pred. No. 35;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 8
 |||||
 Db 141 TVAGNVLT 148

RESULT 7

AB3218
 2-hydroxyacid dehydrogenase Atu5474 [imported] - Agrobacterium tumefaciens (strain C58,

C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB3218
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3218
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-311 <KUR>
A;Cross-references: UNIPROT:Q8UJK3; GB:AE008687; PIDN:AAL46160.1; PID:gl7743930; GSPDB:
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5474
A;Genome: plasmid
C;Superfamily: phosphoglycerate dehydrogenase

Query Match 72.3%; Score 34; DB 2; Length 311;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSGNLTIR 10
:|||||
Db 288 VAGNLTIR 296

RESULT 8
G85835
hypothetical protein yreB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: G85835
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G85835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <STO>
A;Cross-references: UNIPROT:Q9CEZ4; GB:AE005176; PID:gl2724702; PIDN:AAK05785.1; GSPDB:
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yreB

Query Match 72.3%; Score 34; DB 2; Length 314;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSGNLTIR 9
:|||||
Db 93 ISGNLTIR 100

RESULT 9
A85989
hypothetical protein Z4604 [imported] - Escherichia coli (strain O157:H7, substrain ED19
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A85989
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85989
A;Status: preliminary
A;Molecule type: DNA

Query Match 70.2%; Score 33; DB 1; Length 144;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
:|||||
Db 79 TVSGGIITVR 88

RESULT 10
P91143
hypothetical protein ECs4118 [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F91143
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91143
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1266 <HAY>
A;Cross-references: UNIPROT:Q8X9D5; GB:BA000007; PIDN:BA837541.1; PID:gl3363591; GSPDB:
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECs4118
C;Superfamily: Escherichia coli hypothetical protein yhdp

Query Match 72.3%; Score 34; DB 2; Length 1266;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
:|||||
Db 1017 TISGNTLTL 1025

RESULT 11
TPBPPI
tail fiber protein R - phage P1
C;Species: phage P1
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: JS0460
R;Guidolin, A.; Zingg, J.M.; Arber, W.
Gene 76, 239-243, 1989
A;Title: Organization of the bacteriophage P1 tail-fibre operon.
A;Reference number: PS0109; MUID:89326122; PMID:2526777
A;Accession: JS0460
A;Molecule type: DNA
A;Residues: 1-144 <GUI>
A;Cross-references: UNIPROT:P22946; GB:M2S470; NID:G341349; PIDN:AAAS8777.1; PID:G538421
C;Genetics:
A;Gene: R
C;Superfamily: phage P1 tail fiber protein R
C;Keywords: tail fiber

Query Match 70.2%; Score 33; DB 1; Length 144;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
:|||||
Db 79 TVSGGIITVR 88

RESULT 12

S18683
gene R protein - Escherichia coli plasmid p15B
C:Species: Escherichia coli
C:Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S18683
R;Sandmeier, H.; Iida, S.; Huebner, P.; Hiestand-Nauer, R.; Arber, W.
Nucleic Acids Res. 19, 5831-5838, 1991
A:Title: Gene organization in the multiple DNA inversion region Min of plasmid p15B of E
A:Reference number: S18680; MUID:92051368; PMID:1945872
A:Accession: S18683
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-144 <SAN>
A:Cross-references: UNIPROT:Q47426; EMBL:X62121; NID:g42224; PIDN:CAA44046.1; PID:g42228
C:Genetics:
A:Gene: R
A:Genome: plasmid
C:Superfamily: phage P1 tail fiber protein R

Query Match 70.2%; Score 33; DB 2; Length 144;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
| | | | | | | | | |
Db 79 TYSGGHTVR 88

RESULT 13

G95241
MATE efflux family protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Elsen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <KUR>
A:Cross-references: UNIPROT:Q97NG5; GB:AE005672; PIDN:AAK76128.1; PID:g14973575; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2065

Query Match 70.2%; Score 33; DB 2; Length 411;
Best Local Similarity 66.7%; Pred. No. 95;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
| | | | | | | | | |
Db 30 SVAGNIITI 38

RESULT 14

B98106
hypothetical protein MATE transporter [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B98106
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; B
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: B98106
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <KUR>
A:Cross-references: UNIPROT:Q8DN77; GB:AE007317; PIDN:AAL00679.1; PID:g15459568; GSPDB:G
C:Genetics:
A:Gene: MATE transporter

Query Match 70.2%; Score 33; DB 2; Length 426;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
| | | | | | | | | |
Db 45 SVAGNIITI 53

RESULT 15

F85253
hypothetical protein AT4G22170 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85253
R;anonymus, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: F85253
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <STO>
A:Cross-references: UNIPROT:Q9SUG4; GB:NC_001268; NID:g7269062; PIDN:CAB79172.1; GSPDB:G
C:Genetics:
A:Gene: AT4G22170
A:Map position: 4
C:Superfamily: Arabidopsis thaliana hypothetical protein T12H17.50

Query Match 70.2%; Score 33; DB 2; Length 428;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
| | | | | | | | | |
Db 316 TVTGNILRVQ 325

Search completed: September 11, 2005, 01:43:55
Job time : 4.80952 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:20:48 ; Search time 13.2381 Seconds
(without alignments)
386.822 Million cell updates/sec

Title: US-09-529-206E-4_COPY_127_136
Perfect score: 47
Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	180	1 CTG1_HUMAN	P78358 homo sapien
2	40	85.1	141	2 Q67QW2	Q67QW2 symbiobacte
3	39	83.0	142	2 Q9NV13	Q9NV13 homo sapien
4	38	80.9	322	1 LIPA_RH1ET	O05941 rhizobium e
5	37	78.7	250	2 Q8G743	Q8G743 bifidobacte
6	36	76.6	245	2 Q64327	Q64327 bacterioph
7	36	76.6	318	2 Q8EAQ4	Q8EAQ4 shewanella
8	36	76.6	323	1 LIPA_AGR75	Q8UFG1 agrobacteri
9	36	76.6	352	2 Q9YH4	Q9YH4 lampetra fl
10	36	76.6	450	2 Q9R191	Q9R191 streptomyc
11	35	74.5	143	1 IEA2_HUMAN	Q14657 homo sapien
12	35	74.5	144	2 Q8A9J8	Q8A9J8 bacteroides
13	35	74.5	335	2 Q932F0	Q932F0 staphylococ
14	35	74.5	335	2 Q99VV7	Q99VV7 staphylococ
15	35	74.5	335	2 Q7AIK9	Q7AIK9 staphylococ
16	35	74.5	335	2 Q6BG66	Q6BG66 staphylococ
17	35	74.5	335	2 Q6GJ06	Q6GJ06 staphylococ
18	35	74.5	336	2 Q8CQ35	Q8CQ35 staphylococ
19	35	74.5	391	2 Q6LJS0	Q6LJS0 photobacter
20	35	74.5	674	2 Q6NRP9	Q6NRP9 xenopus lae
21	35	74.5	674	2 Q6NRP9	Q6NRP9 xenopus lae
22	35	74.5	674	2 Q9PT82	Q9PT82 xenopus lae
23	35	74.5	674	2 Q9PT83	Q9PT83 xenopus lae
24	35	74.5	742	2 Q8T4D0	Q8T4D0 drosophila
25	35	74.5	742	2 Q9VS00	Q9VS00 drosophila
26	35	74.5	907	2 Q9NEG0	Q9NEG0 drosophila
27	35	74.5	947	2 Q93FV1	Q93FV1 bacteroides
28	35	74.5	986	2 Q6C9K2	Q6C9K2 varrowia li
29	35	74.5	1086	2 Q8MR5	Q8MR5 drosophila
30	35	74.5	3215	2 Q8IRV7	Q8IRV7 drosophila
31	35	74.5	4117	2 Q8IRV9	Q8IRV9 drosophila

32	35	74.5	4179	2 Q9W4Y4	Q9W4Y4 drosophila
33	35	74.5	4223	2 Q8MPN3	Q8MPN3 drosophila
34	35	74.5	4228	2 Q8IRV8	Q8IRV8 drosophila
35	35	74.5	4684	2 Q6LJR7	Q6LJR7 photobacter
36	34	72.3	99	2 Q97675	Q97675 sus scrofa
37	34	72.3	131	1 FABA_PIG	Q97788 sus scrofa
38	34	72.3	177	1 RL6_BACST	P02391 bacillus st
39	34	72.3	244	1 IF6_SCHPO	O94476 schizosacch
40	34	72.3	305	2 Q8VGG6	Q8VGG6 mus musculu
41	34	72.3	311	2 Q8UJK3	Q8UJK3 agrobacteri
42	34	72.3	314	1 OR23_MOUSE	Q8V099 mus musculu
43	34	72.3	314	1 OR25_MOUSE	Q8V097 mus musculu
44	34	72.3	314	1 OR28_MOUSE	Q8V094 mus musculu
45	34	72.3	314	1 OR32_MOUSE	Q8Vfd2 mus musculu

ALIGNMENTS

RESULT 1
CTG1_HUMAN STANDARD; PRT; 180 AA.
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1)
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA Chen Y.-T., Scanlan M.J., Sahin U., Tueraci O., Gure A.O., Tsang S., Williamson B., Stockert E., Pfeundscher M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected by autologous antibody screening."
RL Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Melanoma;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen E., Boon T.;
RT "LAG-1, a new gene with tumor specificity."
RL Int. J. Cancer 76:903-908(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98430682; PubMed=9759882;
RA Wang R.-F., Johnson S.L., Zeng G., Topalian S.L., Schwartzentruber D.J., Rosenberg S.A.;
RT "A breast and melanoma-shared tumor antigen: T cell responses to antigenic peptides translated from different open reading frames."
RL J. Immunol. 161:3596-3606(1998).
CC -1- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in uterine myometrium.
CC -1- SIMILARITY: Belongs to the CTAG family.
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CC -----
CC EMBL: U07459; AAB49693.1; -
CC EMBL: A003149; CAA05908.1; -
CC EMBL: AF038567; AAD05202.1; -
CC Genbank: HGNC:2491; CTAG1B.

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DR MM; 300156; -.
KW Antigen; Transmembrane.
FT DOMAIN 5 82 Gly-rich.
FT TRANSMEM 156 172 Potential.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C38BE1569 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 127 TVSGNLTIR 136
|||||

RESULT 2
ID O67QW2 PRELIMINARY; PRT; 141 AA.
AC Q67QW2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hsp20 family heat shock protein.
GN ORFNames=STH946;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IAM14863;
RA Ueda K., Yanashita A., Ishikawa J., Shimada M., Watsui T.,
RT Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Complete genome sequence of an uncultured bacterium Symbiobacterium
RT thermophilum.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006840; BAD3931.1; -.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR02068; Hsp20.
DR Pfam; PF00011; HSP20; 1.
DR PROSITE; PS01031; HSP20; 1.
KW Heat shock.
SQ SEQUENCE 141 AA; 15725 MW; C7BA8A8CFC50FD36 CRC64;

Query Match 85.1%; Score 40; DB 2; Length 141;
Best Local Similarity 80.0%; Pred. No. 6.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 67 TVDGNLTIR 76
|||||

RESULT 3
ID Q9NY13 PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein LAGE-2 (Fragment).
GN Name=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Lethe B.G.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275978; CAB76945.1; -.
KW Hypothetical protein.

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FT NON_TER 1 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 83.0%; Score 39; DB 2; Length 142;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
Db 101 TVSGNLTIR 109
|||||

RESULT 4
LIPA_RHIET
ID LIPA_RHIET STANDARD; PRT; 322 AA.
AC O05941;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipoyl synthase (EC 2.8.1.-) (Lipoic acid synthase) (Lipoate synthase)
DE (lipoyl-acyl-carrier protein synthase) (Sulfur insertion protein lipa)
DE (lip-syn).
GN Name=lipA;
OS Rhizobium etli.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CE3;
RX MEDLINE=97286510; PubMed=9141657; DOI=10.1016/S0378-1097(97)00069-4;
RA Tate R., Riccio A., Iaccarino M., Patriarca E.J.;
RT "Cloning and transcriptional analysis of the lipA (lipoic acid
RT synthetase) gene from Rhizobium etli.";
RL FEMS Microbiol. Lett. 149:165-172(1997).
CC -!- FUNCTION: Catalyzes the radical-mediated insertion of two sulfur
CC atoms into an acyl carrier protein (ACP) bound to an octanoyl
CC group to produce a lipoyl group (By similarity).
CC -!- CATALYTIC ACTIVITY: octanoyl-[acyl-carrier protein] + 2 sulfurs =
CC lipoyl-[acyl-carrier protein].
CC -!- COFACTOR: Binds 1 4Fe-4S cluster per subunit, and S-adenosyl-L-
CC methionine (AdoMet) used for 5'-deoxyadenosyl radical generation
CC (By similarity).
CC -!- PATHWAY: Lipoate biosynthesis; sulfur-insertion step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the biotin and lipoic acid synthetases
CC family. LipA subfamily.
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CC -----
CC EMBL; Y11708; CAA72400.1; -.
DR HAMAP; MF_00206; -.
DR InterPro; IPR006638; Elp3/MiaB/NifB.
DR InterPro; IPR003698; Lipoate synth.
DR InterPro; IPR007197; Radical_SAM.
DR Pfam; PF04055; Radical_SAM; 1.
DR SMART; SM00729; Elp3; 1.
DR TIGRFAMs; TIGR00510; lipA; 1.
DR 4Fe-4S; Iron; Iron-sulfur; Metal-binding; Transferase.
KW METAL 87 87 Iron-sulfur (Potential).
FT METAL 91 91 Iron-sulfur (Potential).
FT METAL 94 94 Iron-sulfur (Potential).
RN [1]
SQ SEQUENCE 322 AA; 36297 MW; 45E7185215486847 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 322;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 TVSGNLTIR 10
||:|||||:
Db 188 TVAGNLTIR 197

RESULT 5
Q8G743 ID Q8G743 PRELIMINARY; PRT; 250 AA.
AC Q8G743
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Possible cobyric acid synthase CobQ.
GN OrderedLocusNames=BL0429;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaheen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AF014661; AN24266.1; -.
KW Complete proteome.
SQ SEQUENCE 250 AA; 27653 MW; 7577954A609689CF CRC64;

Query Match 78.7%; Score 37; DB 2; Length 250;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGNLTIR 10
||:|||||:
Db 21 SGNLTIR 28

RESULT 6
O64327 ID O64327 PRELIMINARY; PRT; 245 AA.
AC O64327
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gp13.
GN Names=gene 13;
OS Bacteriophage N15.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=40631;
RN [1]
RP SEQUENCE FROM N.A.
RA Hendrix R.W., Ravin V.K., Casjens S.R., Ford M.E., Ravin N.V.,
RA Smirnov I.K.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF064539; AAC19050.1; -.
DR PIR; T13099; T13099.
DR InterPro; IPR003343; Big 2.
DR InterPro; IPR008964; Invasin_intimin.
DR Pfam; PF02368; Big 2; 1.
DR SMART; SM00635; BID 2; 1.
SQ SEQUENCE 245 AA; 25571 MW; 2CC941997C103FD3 CRC64;

Query Match 76.6%; Score 36; DB 2; Length 245;
Best Local Similarity 77.8%; Pred. No. 71;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9

Db 209 TVSGNLTIR 217

RESULT 7
Q8EAQ4 ID Q8EAQ4 PRELIMINARY; PRT; 318 AA.
AC Q8EAQ4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SO3842.
GN OrderedLocusNames=SO3842;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.P., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Claydon R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imbraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AS015817; AN56819.1; -.
DR TIGR; SO3842; -.
KW Complete proteome.
SQ SEQUENCE 318 AA; 34113 MW; 0A0B7165033B6FCF CRC64;

Query Match 76.6%; Score 36; DB 2; Length 318;
Best Local Similarity 87.5%; Pred. No. 92;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 8
||:|||||:
Db 153 TVSGNLTIR 160

RESULT 8
LIPA AGRTS ID LIPA AGRTS STANDARD; PRT; 323 AA.
AC Q8UFG1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipoyl synthase (EC 2.8.1.-) (lipoyl acid synthase) (Lipoate synthase)
DE (lipoyl-acyl-carrier protein synthase) (Sulfur insertion protein lipA)
DE (lip-syn).
GN Name=lipA; OrderedLocusNames=Atu1436, AGR_C.2646;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1065804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayvan T., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon D.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Perry M.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Dolan M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Putative odorant receptor LOR3.
OS Lampetra fluviatilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
NCBI_TaxID=7748;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory;
RX MEDLINE=99043746; PubMed=9828044;
RY DOI=10.1002/(SICI)1097-4695(19981115)37:3<383::AID-NEU4>3.3.CO;2-4;
RA Berghard A., Dryer L.;
RT "A novel family of ancient vertebrate odorant receptors.";
RL J. Neurobiol. 37:383-392(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF069546; AAC82381.1; .
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004952; F:dopamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000925; Dopamine receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7cm_1; 1.
DR PRINTS; PR00242; DOPAMINER.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS0037; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40276 MW; 6366743DCFFA9F4E CRC64;

Query Match 76.6%; Score 36; DB 2; Length 352;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 TVSGNIIIT 9
|| |||||
Db 45 TVVGNIIIT 53

RESULT 10
Q9RJ91 PRELIMINARY; PRT; 450 AA.
ID Q9RJ91 AC
Q9RJ91 AC
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Secretd endo-1,4-beta-xylanase (EC 3.2.1.8).
GN ORFNames=SCF91.34c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.P., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson S.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RP "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- SIMILARITY: Belongs to cellulase family F (family 10 of glycosyl
CC hydrolases).
DR EMBL; AL939106; CAB61191.1; .
DR HSSP; P26514; 1E0W.

DR GO: 0004553; F: hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.
DR GO: 0005975; P: carbohydrate metabolism; IEA.
DR InterPro: IPR001919; Bac_cellose-bind.
DR InterPro: IPR008965; Cellul_bind.
DR InterPro: IPR001000; Glyco_Hydro_10.
DR Pfam: PF00553; CBM_2; 1.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR PRINTS: PR00134; GLHYDRASE10.
DR SMART: SM00633; CBD II; 1.
DR SMART: SM00633; Glyco_10; 1.
DR PROSITE: PS00591; GLYCOSYL HYDROL F10; 1.
KW Complete proteome; Glycosidases; Hydrolase; Xylan degradation.
SQ SEQUENCE 450 AA; 47090 MW; E2FF6A36EC39B6AE CRC64;

Query Match 76.5%; Score 36; DB 2; Length 450;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
| | | | | | | | | |
Db 405 TVSGNVTIR 414

RESULT 11
IBAZ_HUMAN STANDARD; PRT; 143 AA.
ID IBA2_HUMAN
AC Q14657; Q81278;
DT 01-NOV-1997 (Rel. 35, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE IBA2 protein (ESO-3 protease) (DXS9879E).
GN Name=IBA2; Synonyms=ESO3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 2-143 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=96374823; PubMed=8786131; DOI=10.1006/geno.1996.0293;
RA Faranda S., Frattini A., Zucchi I., Patrosso C., Milanesi L.,
RA Montagna C., Vezzoni P.;
RT "Characterization and fine localization of two new genes in Xq28 using
RT the genomic sequence/EST database screening approach.";
RL Genomics 34:323-327(1996).
RN [3]
RP IDENTIFICATION, AND TISSUE SPECIFICITY.
RX PubMed=12384295;
RA Alpen B., Guere A.O., Scanlan M.J., Old L.J., Chen Y.-T.;

RT "A new member of the NY-ESO-1 gene family is ubiquitously expressed in
RT somatic tissues and evolutionarily conserved.";
RL Gene 297:141-149(2002).
CC - TISSUE SPECIFICITY: Ubiquitous.
CC - SIMILARITY: Belongs to the CTAG family.
CC - CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 54.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: BC015744; AAH15744.2; -.
DR EMBL: BC062330; AAH62330.1; -.
DR EMBL: X92896; CAA63489.1; ALT_FRAME.
DR MIM: 300060; -.
SQ SEQUENCE 143 AA; 14804 MW; AD164559371449P8 CRC64;

Query Match 74.5%; Score 35; DB 1; Length 143;
Best Local Similarity 70.0%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
| | | | | | | | | |
Db 98 TVSGRILVVR 107

RESULT 12
OBA9J8 PRELIMINARY; PRT; 144 AA.
ID OBA9J8
AC OBA9J8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BT0817;
OC Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL: AE016929; AAO75924.1; -.
DR InterPro: IPR007298; Nlpe.
DR Pfam: PF04170; Nlpe; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 144 AA; 15781 MW; AB28935887F6976B CRC64;

Query Match 74.5%; Score 35; DB 2; Length 144;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
| | | | | | | | | |
Db 96 TVSGNLTIR 105

RESULT 13
O932F0 PRELIMINARY; PRT; 335 AA.
ID O932F0
AC O932F0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Low-affinity inorganic phosphate transporter.
GS OrderedLocusNames=SAV0664;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaiko C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003360; BAB56826.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005315; F:inorganic phosphate transporter activity; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001204; Phos_transporter.
DR Pfam; PF01384; PHO4; 1.
KW Complete proteome.
SQ SEQUENCE 335 AA; 35604 MW; 9135CAB8343FD628 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 335;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
DB 245 TVGGNIMKIR 254

RESULT 14
Q99VV7 PRELIMINARY; PRT; 335 AA.
AC Q99VV7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SA0619 protein.
GN OrderedLocusNames=SA0619;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N315;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaiko C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003360; BAB56826.1; -.
DR PIR; A89837; A89837.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005315; F:inorganic phosphate transporter activity; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001204; Phos_transporter.
DR Pfam; PF01384; PHO4; 1.
KW Complete proteome.
SQ SEQUENCE 335 AA; 35588 MW; 9121CBF8343FD628 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 335;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
DB 245 TVGGNIMKIR 254

RESULT 15
Q7AIK9 PRELIMINARY; PRT; 335 AA.
AC Q7AIK9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MW0626 protein.
GN OrderedLocusNames=MW0626;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004824; BAB94491.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005315; F:inorganic phosphate transporter activity; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001204; Phos_transporter.
DR Pfam; PF01384; PHO4; 1.
KW Complete proteome.
SQ SEQUENCE 335 AA; 35588 MW; 9121CBF8343FD628 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 335;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
DB 245 TVGGNIMKIR 254

Search completed: September 11, 2005, 01:42:53
Job time : 16.2381 secs

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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:30:14 ; Search time 3.66667 Seconds
(without alignments)
203.588 Million cell updates/sec

Title: US-09-529-206E-4_COPY_127_136

Perfect score: 47

Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	18	3 US-09-359-503-9	Sequence 9, Appli
2	47	100.0	18	3 US-09-359-503-13	Sequence 13, Appli
3	47	100.0	18	4 US-09-165-546D-9	Sequence 9, Appli
4	47	100.0	18	4 US-09-165-546D-13	Sequence 13, Appli
5	47	100.0	18	4 US-09-408-036B-8	Sequence 8, Appli
6	47	100.0	18	4 US-09-408-036B-12	Sequence 12, Appli
7	47	100.0	18	2 US-08-791-495-9	Sequence 9, Appli
8	47	100.0	180	3 US-08-937-263B-8	Sequence 8, Appli
9	47	100.0	180	4 US-09-751-798-8	Sequence 8, Appli
10	47	100.0	180	4 US-09-392-714-25	Sequence 25, Appli
11	47	100.0	180	4 US-09-165-546D-15	Sequence 15, Appli
12	47	100.0	180	4 US-09-341-829A-9	Sequence 9, Appli
13	47	100.0	180	4 US-09-849-602-30	Sequence 30, Appli
14	42	89.4	9	4 US-09-344-040C-125	Sequence 125, App
15	42	89.4	9	4 US-09-833-039A-125	Sequence 125, App
16	38	80.9	9	4 US-09-344-040C-120	Sequence 120, App
17	38	80.9	9	4 US-09-833-039A-120	Sequence 120, App
18	38	80.9	180	2 US-08-791-495-7	Sequence 7, Appli
19	38	80.9	180	4 US-09-341-829A-7	Sequence 7, Appli
20	37	78.7	574	4 US-09-248-796A-16162	Sequence 16162, A
21	35	74.5	342	3 US-09-134-001C-5428	Sequence 5428, Ap
22	34	72.3	149	4 US-09-540-236-2614	Sequence 2614, Ap
23	34	72.3	177	4 US-09-732-210-1076	Sequence 1076, Ap
24	34	72.3	185	4 US-09-270-767-58027	Sequence 58027, A
25	34	72.3	379	4 US-09-270-767-42707	Sequence 42707, A
26	33	70.2	97	1 US-08-118-270-329	Sequence 329, App
27	33	70.2	97	5 PCT-US93-08528-329	Sequence 329, App

28	33	70.2	109	4 US-09-341-461-35	Sequence 35, Appli
29	33	70.2	362	3 US-09-134-001C-5209	Sequence 5209, Ap
30	33	70.2	379	1 US-08-118-270-32	Sequence 32, Appli
31	33	70.2	379	5 PCT-US93-08528-32	Sequence 32, Appli
32	33	70.2	426	4 US-09-583-110-4783	Sequence 4783, Ap
33	33	70.2	434	4 US-09-107-433-3247	Sequence 3247, Ap
34	33	70.2	470	3 US-09-292-071-25	Sequence 25, Appli
35	33	70.2	470	3 US-09-292-069A-25	Sequence 25, Appli
36	33	70.2	470	4 US-09-767-013-25	Sequence 25, Appli
37	33	70.2	470	4 US-09-292-072-25	Sequence 25, Appli
38	33	70.2	471	1 US-07-817-920-8	Sequence 8, Appli
39	33	70.2	471	1 US-07-996-772A-11	Sequence 11, Appli
40	33	70.2	471	1 US-08-370-542-7	Sequence 7, Appli
41	33	70.2	471	1 US-08-117-006-8	Sequence 8, Appli
42	33	70.2	471	1 US-08-216-594-8	Sequence 8, Appli
43	33	70.2	471	1 US-08-542-358-7	Sequence 7, Appli
44	33	70.2	471	2 US-08-244-434-2	Sequence 2, Appli
45	33	70.2	471	3 US-09-018-351-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

to NY-

; TOPOLOGY: linear
US-09-359-503-9

Query Match 100.0%; Score 47; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 2

US-09-359-503-13
; Sequence 13, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-359-503-13

Query Match 100.0%; Score 47; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 3

US-09-165-546D-9
; Sequence 9, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; APPLICANT: Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-165-546D-9

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 4

US-09-165-546D-13
; Sequence 13, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; APPLICANT: Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue

;; CITY: New York City
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10158
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Word
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/165,546D
;; FILING DATE: 02-Oct-1998
;; CLASSIFICATION: 530
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/062,422
;; FILING DATE: April 17, 1998
;; APPLICATION NUMBER: 08/937,263
;; FILING DATE: September 15, 1997
;; APPLICATION NUMBER: US 08/725,182
;; FILING DATE: October 3, 1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 6723832man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 318-3000
;; TELEFAX: (212) 318-3400
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-165-546D-13

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
|||||
DB 1 TVSGNLTIR 10

RESULT 5
US-09-408-036B-8
; Sequence 8, Application US/09408036B
; Patent No. 6800730
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-8

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
|||||

Db 7 TVSGNLTIR 16

RESULT 6

US-09-408-036B-12
; Sequence 12, Application US/09408036B
; Patent No. 6800730
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-12

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
|||||
DB 1 TVSGNLTIR 10

RESULT 7

US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match          100.0%; Score 47; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 8
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drifhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8

Query Match          100.0%; Score 47; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 9
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
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; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; MOLECULE TYPE: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6525177man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match          100.0%; Score 47; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 10
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-392-714-25

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Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 11
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
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Query Match      100.0%; Score 47; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136
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RESULT 12
US-09-341-829A-9
; Sequence 9, Application US/09341829A
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; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9
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Query Match      100.0%; Score 47; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 13
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseeng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105 (JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30
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Query Match      100.0%; Score 47; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136
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RESULT 14
US-09-344-040C-125
; Sequence 125, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
; TITLE OF INVENTION: Gene, and Uses Thereof
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; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-125

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Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTI 9
Db 1 TVSGNILTI 9

RESULT 15

US-09-833-039A-125
; Sequence 125, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-125

Query Match 89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTI 9
Db 1 TVSGNILTI 9

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Job time : 4.66667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2005, 01:43:05 ; Search time 13.5238 Seconds
(without alignments)
291.657 Million cell updates/sec

Title: US-09-529-206E-4_COPY_127_136

Perfect score: 47
Sequence: 1 TVSGNLTIR 10

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Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	47	100.0	15	18	US-10-182-506A-15
3	47	100.0	15	18	US-10-182-506A-16
4	47	100.0	18	16	US-10-751-088-9
5	47	100.0	18	16	US-10-751-088-13
6	47	100.0	18	16	US-10-851-884-8
7	47	100.0	18	16	US-10-851-884-12
8	47	100.0	18	18	US-10-182-506A-65
9	47	100.0	20	15	US-10-164-121A-35
10	47	100.0	20	15	US-10-164-078A-34
11	47	100.0	20	18	US-10-182-506A-38
					Sequence 17, Appl
					Sequence 15, Appl
					Sequence 16, Appl
					Sequence 9, Appl
					Sequence 13, Appl
					Sequence 8, Appl
					Sequence 12, Appl
					Sequence 65, Appl
					Sequence 35, Appl
					Sequence 34, Appl
					Sequence 38, Appl

12	47	100.0	25	17	US-10-491-891-83	Sequence 83, Appl
13	47	100.0	27	18	US-10-182-506A-7	Sequence 7, Appl
14	47	100.0	27	18	US-10-182-506A-6	Sequence 6, Appl
15	47	100.0	30	15	US-10-296-734-1414	Sequence 1414, Ap
16	47	100.0	54	15	US-10-447-161-140	Sequence 140, App
17	47	100.0	123	16	US-10-777-053-17	Sequence 17, Appl
18	47	100.0	123	16	US-10-837-217-17	Sequence 17, Appl
19	47	100.0	179	16	US-10-777-053-20	Sequence 20, Appl
20	47	100.0	179	16	US-10-837-217-20	Sequence 20, Appl
21	47	100.0	179	17	US-10-482-029-202	Sequence 202, App
22	47	100.0	180	9	US-09-751-798-8	Sequence 8, Appl
23	47	100.0	180	10	US-09-849-602-30	Sequence 30, Appl
24	47	100.0	180	13	US-10-023-182-8	Sequence 8, Appl
25	47	100.0	180	14	US-10-207-655-71	Sequence 71, Appl
26	47	100.0	180	15	US-10-026-066-3	Sequence 3, Appl
27	47	100.0	180	15	US-10-117-937-74	Sequence 74, Appl
28	47	100.0	180	15	US-10-285-027-386	Sequence 386, App
29	47	100.0	180	15	US-10-296-734-832	Sequence 832, App
30	47	100.0	180	15	US-10-188-832-139	Sequence 139, App
31	47	100.0	180	16	US-10-777-053-11	Sequence 11, Appl
32	47	100.0	180	16	US-10-751-088-15	Sequence 15, Appl
33	47	100.0	180	16	US-10-657-022-74	Sequence 74, Appl
34	47	100.0	180	16	US-10-837-217-11	Sequence 11, Appl
35	47	100.0	180	16	US-10-877-373-9	Sequence 9, Appl
36	47	100.0	180	16	US-10-723-860-1270	Sequence 1270, Ap
37	47	100.0	180	17	US-10-871-708-7	Sequence 7, Appl
38	47	100.0	180	18	US-10-895-523-3	Sequence 3, Appl
39	47	100.0	180	18	US-10-182-506A-3	Sequence 3, Appl
40	47	100.0	180	18	US-10-756-149-5024	Sequence 5024, Ap
41	47	100.0	180	20	US-11-067-064-74	Sequence 74, Appl
42	47	100.0	397	9	US-09-821-883-27	Sequence 27, Appl
43	47	100.0	3541	15	US-10-296-734-1454	Sequence 1454, Ap
44	42	89.4	9	10	US-09-833-039-125	Sequence 125, App
45	42	89.4	9	14	US-10-177-277-125	Sequence 125, App

ALIGNMENTS

RESULT 1
US-10-182-506A-17
; Sequence 17, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-17

Query Match 100.0% Score 47; DB 18; Length 14;
Best Local Similarity 100.0%; Pred.No. 0.026; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 TVSGNLTIR 10

Db |||||||
 4 TVSGNLTIR 13

RESULT 2

US-10-182-506A-15
; Sequence 15, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-15

Query Match 100.0%; Score 47; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
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Db 6 TVSGNLTIR 15

RESULT 3

US-10-182-506A-16
; Sequence 16, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-16

Query Match 100.0%; Score 47; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 5 TVSGNLTIR 14

RESULT 4

US-10-751-088-9
; Sequence 9, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; APPLICANT: Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
; USES THEREOF

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10158
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-751-088-9

Query Match 100.0%; Score 47; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 |||||||
Db 7 TVSGNLTIR 16

RESULT 5

US-10-751-088-13
; Sequence 13, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;

```
; Gurg, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
; USES THEREOF
;
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/751.088
; FILING DATE: 02-Jan-2004
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/165.546D
; FILING DATE: 02-Oct-1998
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
;
; INFORMATION FOR SEQ ID NO: 13:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-751-088-13

Query Match 100.0%; Score 47; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.035; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 6
US-10-851-884-8
; Sequence 8, Application US/10851884
; Publication No. US20040214284A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/10/851,884
; PRIOR FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US/09/408,036
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 18
; TYPE: PRT
;
; NUMBER OF SEQ ID NOS: 38
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; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-851-884-8

Query Match 100.0%; Score 47; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.035; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 7
US-10-851-884-12
; Sequence 12, Application US/10851884
; Publication No. US20040214284A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/10/851,884
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US/09/408,036
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-851-884-12

Query Match 100.0%; Score 47; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.035; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 8
US-10-182-506A-65
; Sequence 65, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 18
; TYPE: PRT
;
; NUMBER OF SEQ ID NOS: 38
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-65

Query Match 100.0%; Score 47; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.035; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
| | | | | | | |
Db 7 TVSGNLTIR 16

RESULT 9

US-10-164-121A-35
; Sequence 35, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 35
; LENGTH: 20
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-164-121A-35

Query Match 100.0%; Score 47; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
| | | | | | | |
Db 9 TVSGNLTIR 18

RESULT 10

US-10-164-078A-34
; Sequence 34, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-164-078A-34

Query Match 100.0%; Score 47; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
| | | | | | | |
Db 9 TVSGNLTIR 18

RESULT 11

US-10-182-506A-38
; Sequence 38, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-38

Query Match 100.0%; Score 47; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
| | | | | | | |
Db 2 TVSGNLTIR 11

RESULT 12

US-10-491-891-83
; Sequence 83, Application US/10491891
; Publication No. US20050059107A1
; GENERAL INFORMATION:
; APPLICANT: MAILLERE, BERNARD
; APPLICANT: CASTELLI, FLORENCE
; APPLICANT: BUHOT, CECILE
; APPLICANT: GEORGES, BERTRAND
; TITLE OF INVENTION: METHOD OF SELECTING HLA-DP4 LIGANDS AND THE APPLICATIONS THEREOF
; FILE REFERENCE: 251858USOXPT
; CURRENT APPLICATION NUMBER: US/10/491,891
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: PCT/FR02/03555
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: FR01/13352
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-491-891-83

Query Match 100.0%; Score 47; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.051; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
| | | | | | | |

Db 9 TVSGNLTIR 18

RESULT 13

US-10-182-506A-7
; Sequence 7, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-7

Query Match 100.0%; Score 47; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

Db 15 TVSGNLTIR 24

RESULT 14

US-10-182-506A-6
; Sequence 6, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-6

Query Match 100.0%; Score 47; DB 18; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

Db 17 TVSGNLTIR 26

RESULT 15

US-10-296-734-1414
; Sequence 1414, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1414
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 9
US-10-296-734-1414

Query Match 100.0%; Score 47; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

Db 9 TVSGNLTIR 18

Search completed: September 11, 2005, 02:07:11
Job time : 14.5238 secs

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